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173500

ME

From: Russel, Jeffrey
Sent: Monday, December 05, 2005 4:53 PM
To: STIC-Biotech/ChemLib
Subject: Database Search Request

Requester:
Jeffrey Russel (TC1600)
Art Unit:
1654
Employee Number:
62785
Office Location:
REM 3D19
Phone_Number:
571-272-0969
Mailbox Number:
REM 3C18

Case serial number:
10/789,494
Class / Subclass(es):
NA
Earliest Priority Filing Date:
NA
Format preferred for results:
Diskette

Search Topic Information:

Please Search SEQ ID NO:1 (VITTDSDGNE) and SEQ ID NO:5 (YGWGDGGYGSDS) in STN, in the U.S. patent application sequence databases (pending, published, and issued), and in Geneseq/Uniprot/Pir. Thank you.
Special Instructions and Other Comments:

Checked

JRU
12-14-2005

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DEC - 6 2005
STIC/BIOTECH/ChemLib

Point of Contact:

Searcher: **Alexandra Wacławiw**
Searcher Phone: **CM 1 800 308-4497**
Date Searcher Picked up: **12-8**
Date completed: **12-12**
Searcher Prep Time: **15**
Online Time: **15**

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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(FILE 'HOME' ENTERED AT 08:46:50 ON 12 DEC 2005)

FILE 'REGISTRY' ENTERED AT 08:46:58 ON 12 DEC 2005

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L2 17 SEA ABB=ON PLU=ON YGWGDGGYGSDS/SQSP

FILE 'CAPLUS' ENTERED AT 08:47:44 ON 12 DEC 2005

L3 4 SEA ABB=ON PLU=ON L1
L4 5 SEA ABB=ON PLU=ON L2

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FILE 'REGISTRY' ENTERED AT 08:48:52 ON 12 DEC 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 11 DEC 2005 HIGHEST RN 869700-38-9
DICTIONARY FILE UPDATES: 11 DEC 2005 HIGHEST RN 869700-38-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Structure search iteration limits have been increased. See HELP SLIMITS
for details.

REGISTRY includes numerically searchable data for experimental and
predicted properties as well as tags indicating availability of
experimental property data in the original document. For information
on property searching in REGISTRY, refer to:

<http://www.cas.org/ONLINE/UG/regprops.html>

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CN 1: PN: JP2004339189 PAGE: 8 unclaimed sequence (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 151

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference

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	unclaimed
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HITS AT: 85-94

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 2 OF 6 REGISTRY COPYRIGHT 2005 ACS on STN

RN 714954-20-8 REGISTRY

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 aspartyl-L-seryl-L- α -aspartylglycyl-L-asparaginy- (9CI) (CA INDEX
 NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 10

SEQ 1 VITTDSDGNE

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HITS AT: 1-10

MF C41 H67 N11 O21

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

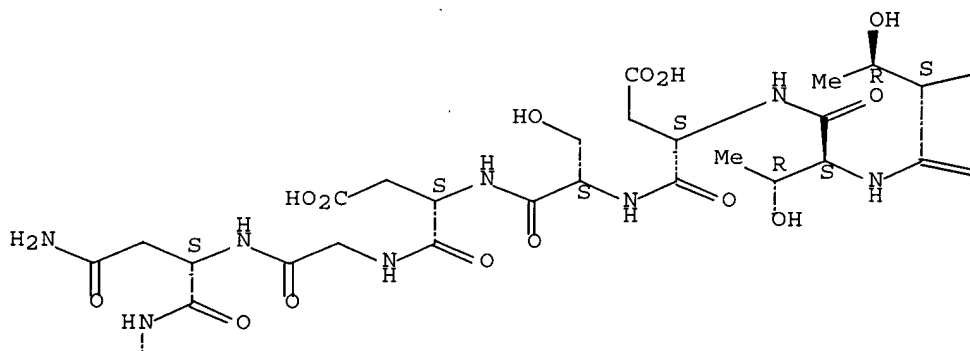
DT.CA Caplus document type: Journal; Patent

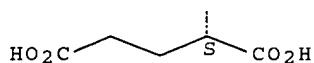
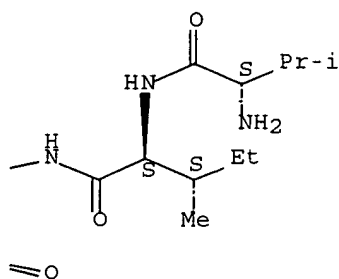
RL.P Roles from patents: BIOL (Biological study); OCCU (Occurrence); PREP
 (Preparation); USES (Uses)

RL.NP Roles from non-patents: BIOL (Biological study); USES (Uses)

Absolute stereochemistry.

PAGE 1-A





PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

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2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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OTHER NAMES:
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HITS AT: 85-94
MF Unspecified
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SR GenBank

L1 ANSWER 4 OF 6 REGISTRY COPYRIGHT 2005 ACS on STN
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CN GenBank AAA27838 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAA27838 (Translated from: GenBank M24222)
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L1 ANSWER 5 OF 6 REGISTRY COPYRIGHT 2005 ACS on STN
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CN Fibroin (silkworm strain p50 heavy chain) (9CI) (CA INDEX NAME)
OTHER NAMES:
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CN GenBank AAF76983
CN GenBank AAF76983 (Translated from: GenBank AF226688)
FS PROTEIN SEQUENCE
SQL 5263

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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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L2 ANSWER 1 OF 17 REGISTRY COPYRIGHT 2005 ACS on STN

RN 803823-78-1 REGISTRY

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CN 13: PN: JP2004339189 PAGE: 9 unclaimed sequence

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SQL 45

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

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Not Given | JP2004339189

| unclaimed

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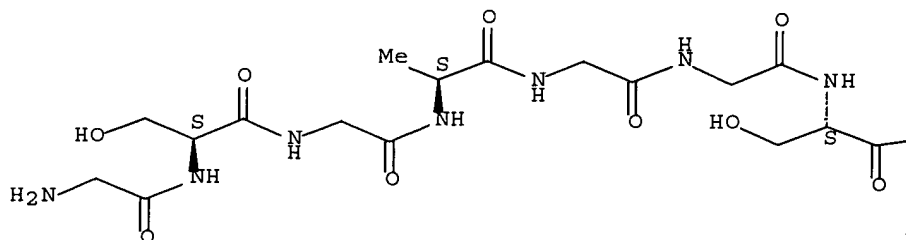
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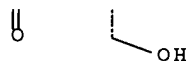
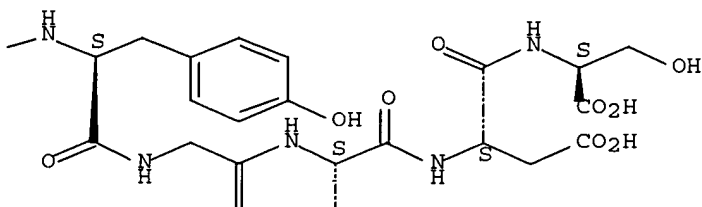
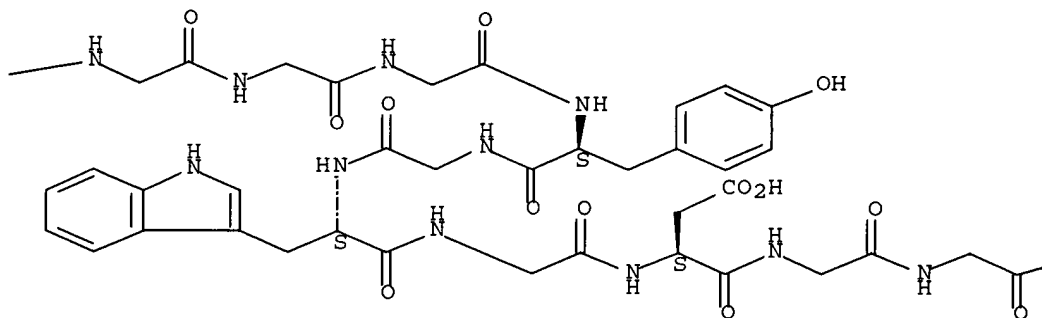
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LC      STN Files:      CA, CAPLUS, USPATFULL
DT.CA      Caplus document type: Patent
RL.P      Roles from patents: PRP (Properties)

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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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OTHER NAMES:

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 21

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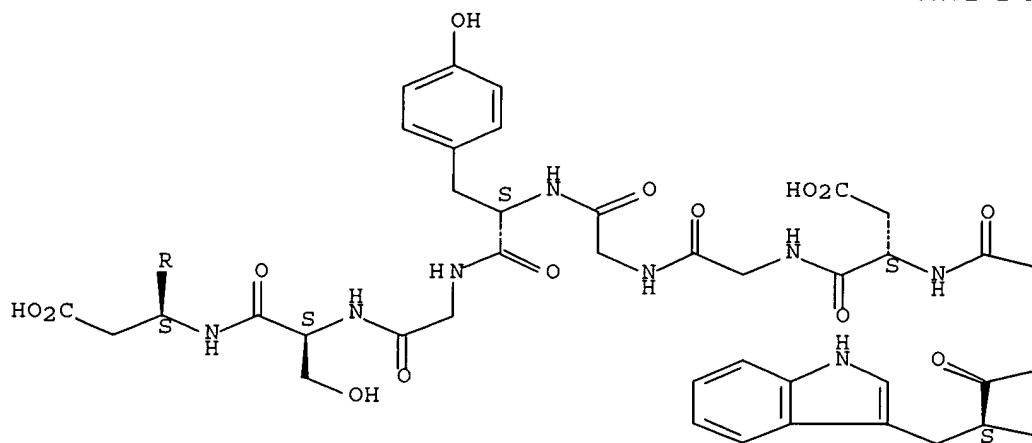
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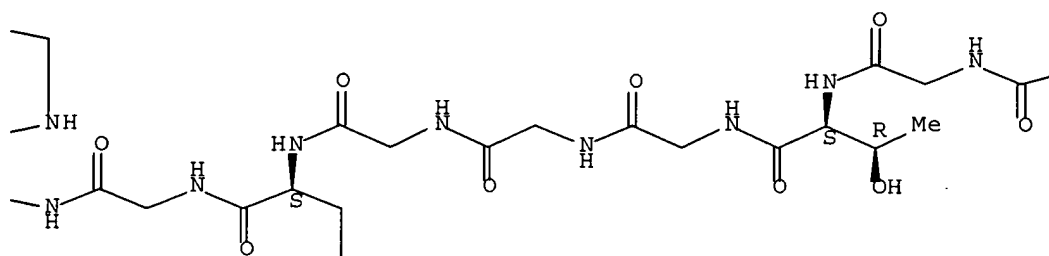
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RL.P Roles from patents: PRP (Properties)

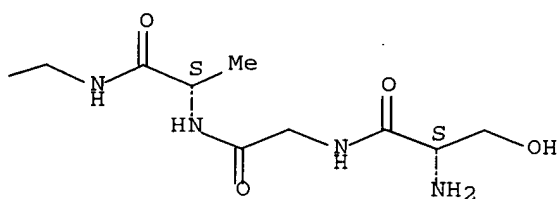
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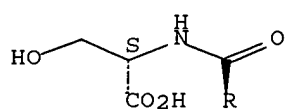
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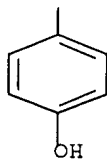


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PAGE 2-A





PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L2 ANSWER 4 OF 17 REGISTRY COPYRIGHT 2005 ACS on STN
RN 803731-40-0 REGISTRY
CN L-Serine, glycyl-L-serylglycyl-L-alanylglycylglycyl-L-
alanylglycylglycylglycyl-L-tyrosylglycyl-L-tryptophylglycyl-L- α -
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(CA INDEX NAME)

OTHER NAMES:

CN 33: PN: JP2004339189 PAGE: 10 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 22

PATENT ANNOTATIONS (PNTE):

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Not Given	JP2004339189 unclaimed PAGE 10
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MF C76 H101 N23 O32

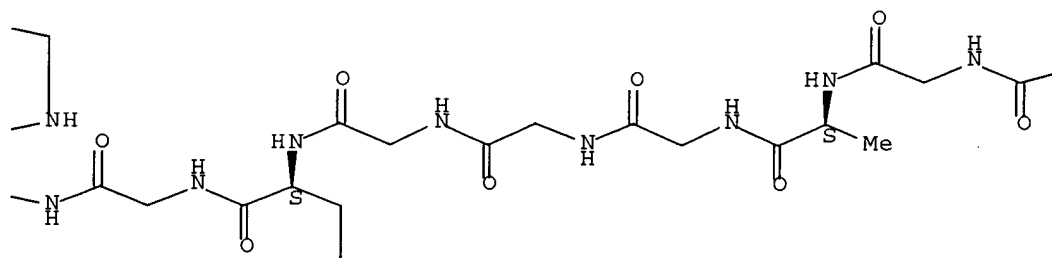
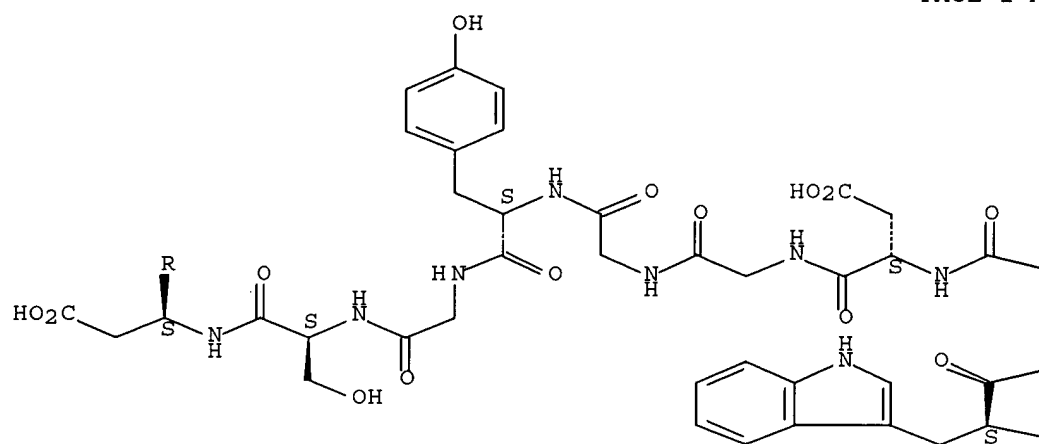
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LC STN Files: CA, CAPLUS, USPATFULL

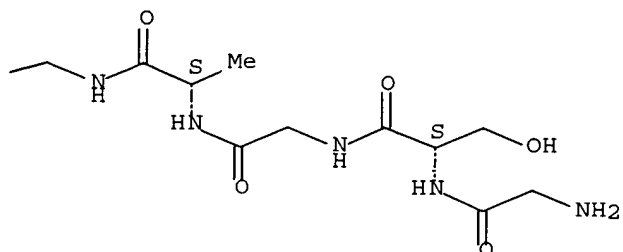
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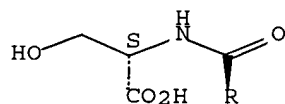
Absolute stereochemistry.



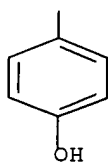
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PAGE 2-A



PAGE 2-B



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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L2 ANSWER 5 OF 17 REGISTRY COPYRIGHT 2005 ACS on STN

RN 803731-38-6 REGISTRY

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(CA INDEX NAME)

OTHER NAMES:

CN 28: PN: JP2004339189 PAGE: 9 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 22

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference

Not Given	JP2004339189
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HITS AT: 11-22

MF C78 H105 N23 O32

SR CA

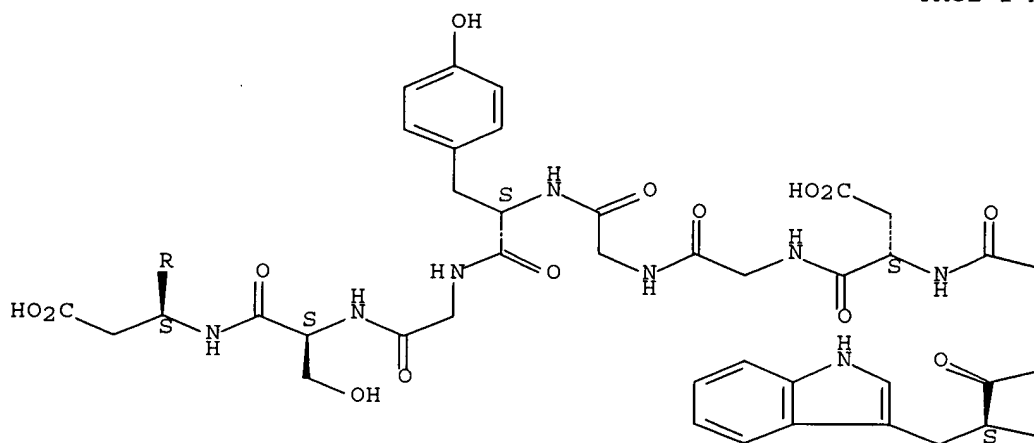
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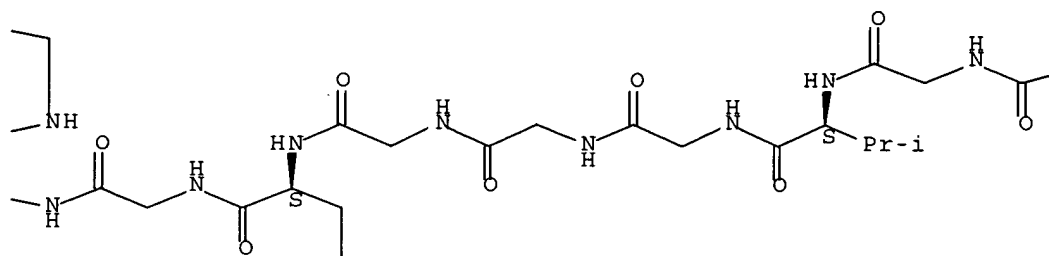
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Absolute stereochemistry.

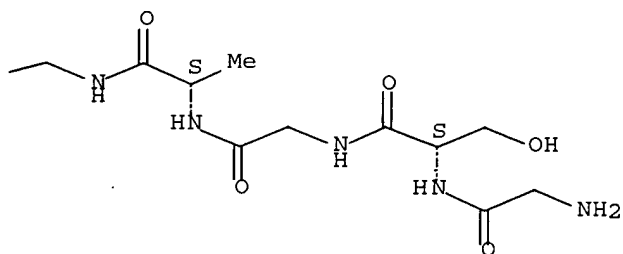
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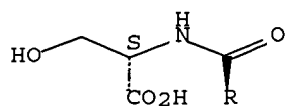
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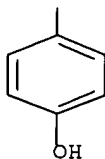


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PAGE 2-A





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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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RN 803731-34-2 REGISTRY
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OTHER NAMES:
CN 25: PN: JP2004339189 PAGE: 9 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 21

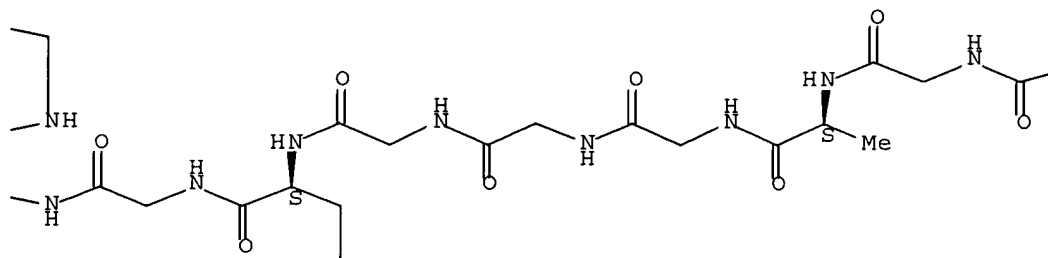
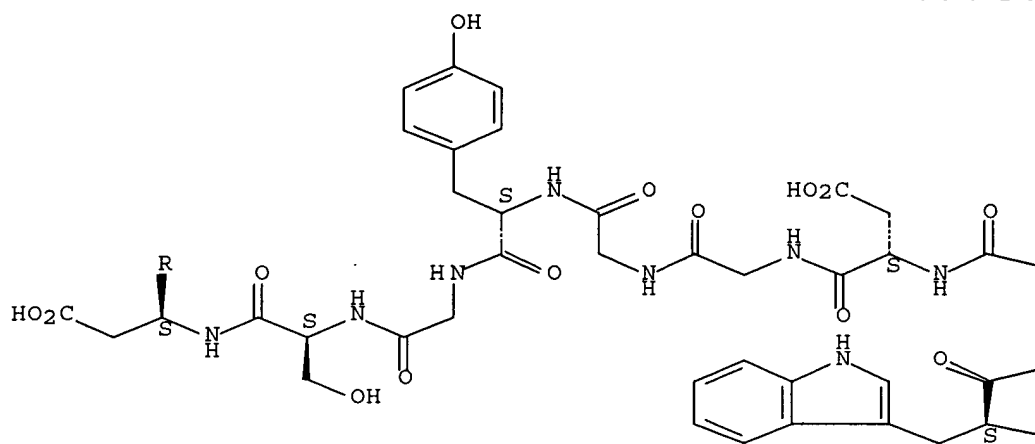
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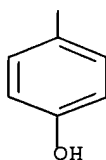
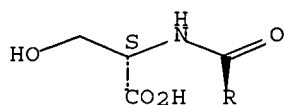
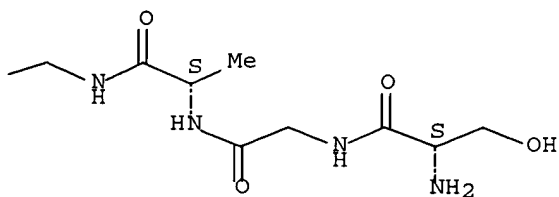
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MF C74 H98 N22 O31
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LC STN Files: CA, CAPLUS, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: PRP (Properties)

Absolute stereochemistry.





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L2 ANSWER 7 OF 17 REGISTRY COPYRIGHT 2005 ACS on STN
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(CA INDEX NAME)

OTHER NAMES:

CN 24: PN: JP2004339189 PAGE: 9 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 22

PATENT ANNOTATIONS (PNTE):

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Source	Reference
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MF C78 H103 N23 O34

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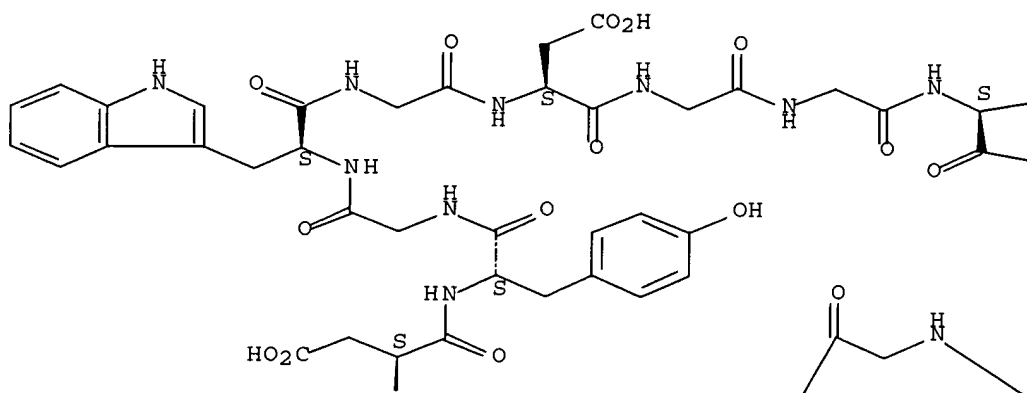
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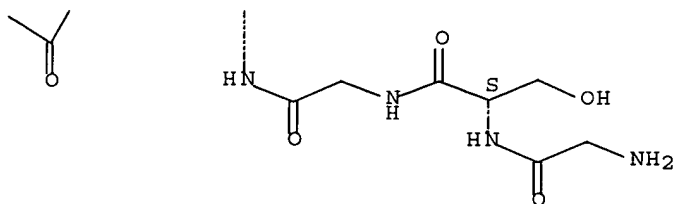
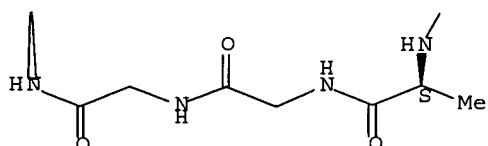
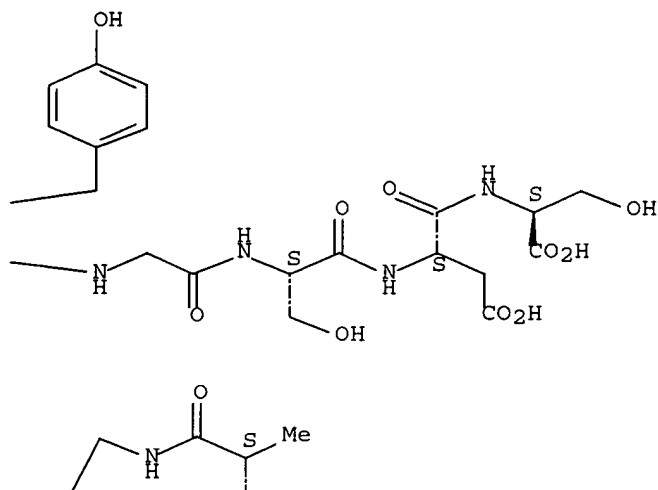
DT.CA Caplus document type: Patent

RL.P Roles from patents: PRP (Properties)

Absolute stereochemistry.

PAGE 1-A





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OTHER NAMES:
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FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 21

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Source	Reference
Not Given	JP2004339189
	unclaimed
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MF C78 H107 N25 O32

SR CA

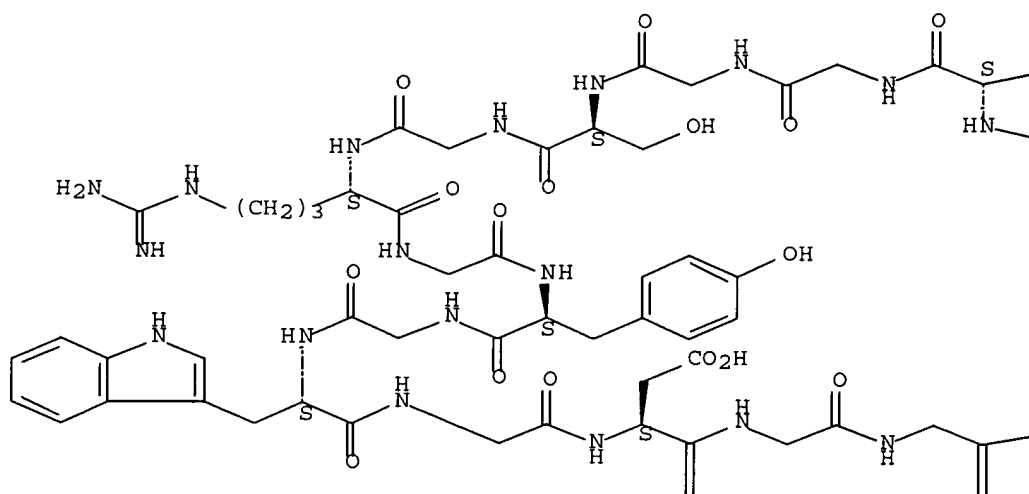
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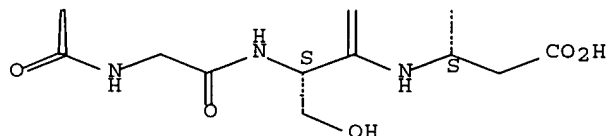
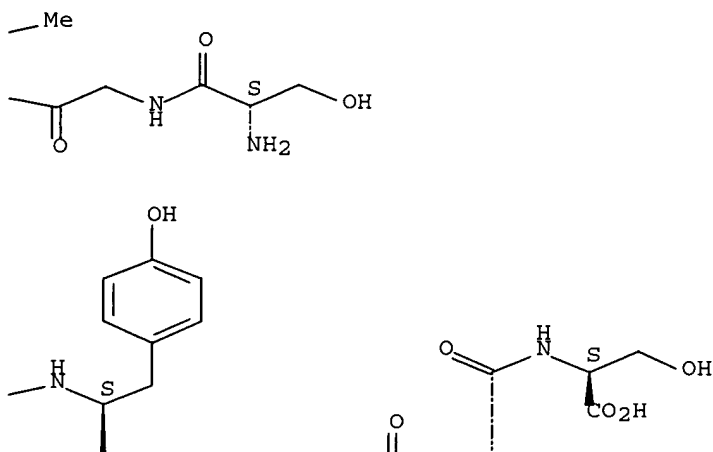
DT.CA Caplus document type: Patent

RL.P Roles from patents: PRP (Properties)

Absolute stereochemistry.

PAGE 1-A





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FS PROTEIN SEQUENCE; STEREOSEARCH
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Source	Reference

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|unclaimed
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SR CA

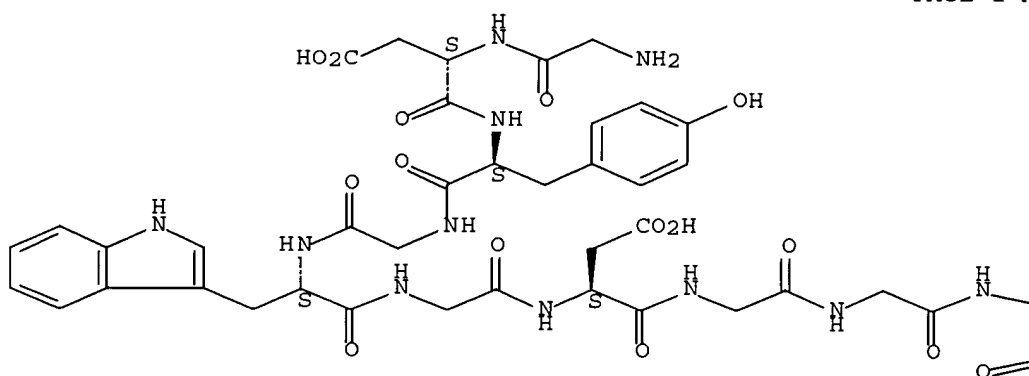
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DT.CA Caplus document type: Patent

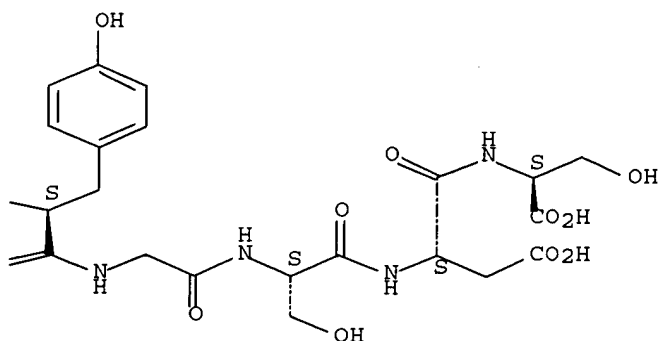
RL.P Roles from patents: PRP (Properties)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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OTHER NAMES:

CN 18: PN: JP2004339189 PAGE: 9 unclaimed sequence
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 SQL 21

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Source	Reference

Not Given	JP2004339189
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MF C74 H98 N22 O32

SR CA

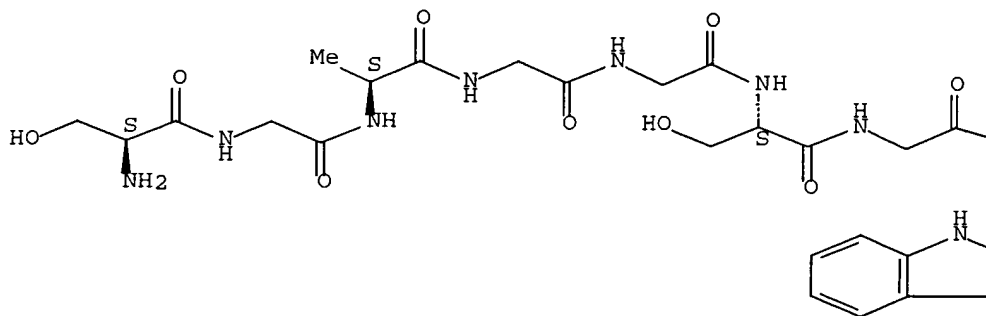
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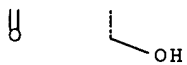
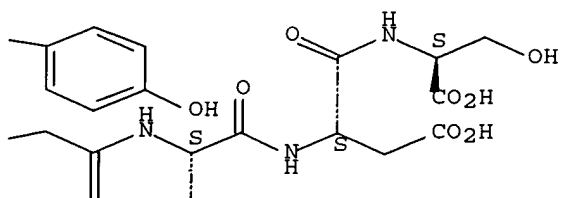
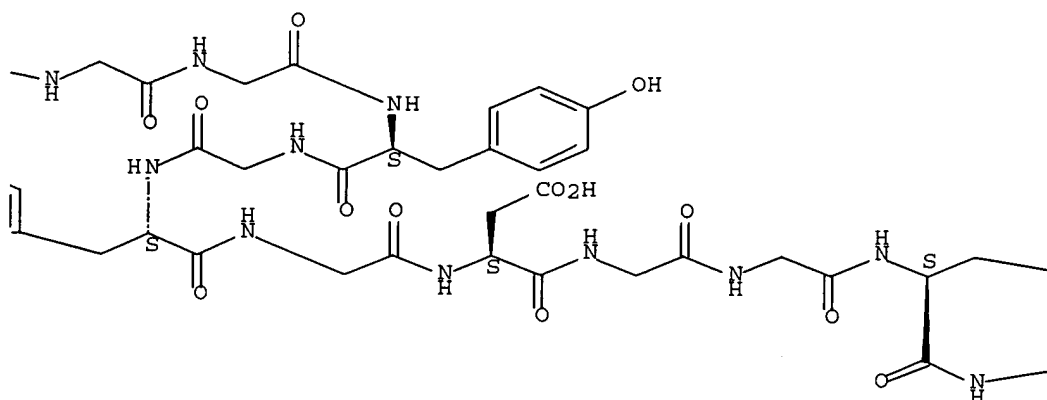
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RL.P Roles from patents: PRP (Properties)

Absolute stereochemistry.

PAGE 1-A





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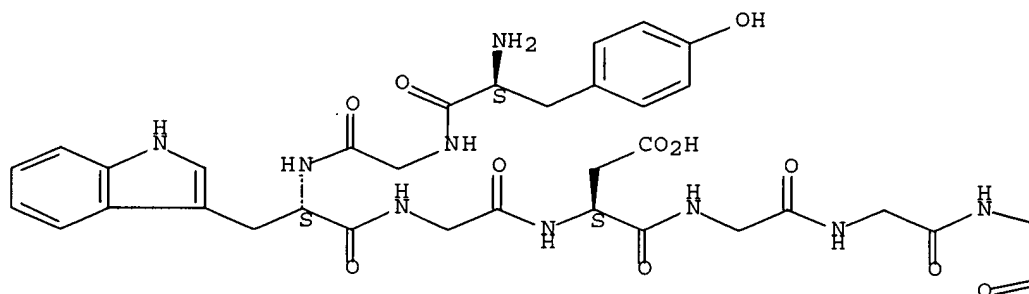
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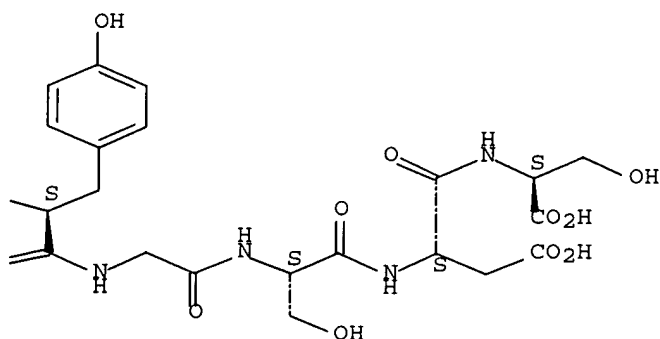
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 DT.CA Caplus document type: Patent
 RL.P Roles from patents: BIOL (Biological study); OCCU (Occurrence); PREP
 (Preparation); USES (Uses)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



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OTHER NAMES:
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FS PROTEIN SEQUENCE
SQL 405

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LC STN Files: CA, CAPLUS
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RN 481611-80-7 REGISTRY
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OTHER NAMES:
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HITS AT: 232-243, 408-419

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CI MAN

SR GenBank

L2 ANSWER 15 OF 17 REGISTRY COPYRIGHT 2005 ACS on STN

RN 404318-03-2 REGISTRY

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OTHER NAMES:

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FS PROTEIN SEQUENCE

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2501 YSWDYSSYG ESAAAAA AAGSGAGGVG GYGGGDGGY GSGSSAAAA
2551 AAAAAARR AGHDRAYGAG SAAAAA AGAGASRPV IYGTDDGFVL
2601 DGGYDSEGA AAAAAA ASSGRSTEG HPLLSICCRP CSHRHSYEAS
2651 RISVH

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HITS AT: 170-181, 328-339, 363-374, 395-406, 427-438, 514-525,
549-560, 581-592, 666-677, 701-712, 733-744, 819-830,
854-865, 886-897, 972-983, 1007-1018, 1039-1050,
1125-1136, 1160-1171, 1224-1235, 1322-1333, 1386-1397,
1472-1483, 1536-1547, 1622-1633, 1686-1697, 1772-1783,
1807-1818, 1839-1850, 1871-1882, 1992-2003, 2027-2038,
2148-2159, 2210-2221, 2433-2444

MF Unspecified

CI MAN
 SR CA
 LC STN Files: CA, CAPLUS
 DT.CA CAplus document type: Journal
 RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L2 ANSWER 16 OF 17 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 336885-96-2 REGISTRY
 CN Fibroin (Antheraea pernyi clone AP2) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank AAC32606
 CN GenBank AAC32606 (Translated from: GenBank AF083334)
 FS PROTEIN SEQUENCE
 SQL 2639

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SEQ      1 MRVIAFVILC CALQYATAKN LRHHDEYVDN HGQLVERFTT RKFHERNAAT
      51 RPHLSGNERL VETIVLEEDP YGHEDIYEED VVIKRVPGAS SSAAAASSAS
     101 AGSGQTIIVE RQASHGAGGA AGAAAGAAAG SSARRGGGFY ETHNSYSSYG
     151 SGSSAAAGS GAGGVGGGYG SDSAAAAAAA AAAASGAGGS GGYGGYSDS
     201 AAAAAAAAAA AAAGSGAGGS GGYGGYGGYG SDSAAAAAAA AAAAAAGSSA
     251 GGAGGGYGWG DGGYGSDSAA AAAAAAAAAA AGSGAGGSGG YGGYGSDSAA
           =====
     301 AAAAAAAAAA AGSSAGGAGG GYGWGDGGYG SDSAAAAAAA AAAAASSGAG
           =====
     351 GRGDGGYGSG GSSAAAAAAA AAAAARRAGH DRAAGSAAAA AAAAAAAAAAS
     401 GAGSGGGYG WGDGGYGSDS AAAAAAAAAA AAAGSGAGGA GGGYGWGDG
           == =====
     451 YGSDSAAAAA AAAAAAASG AGGSGGYGGY GSDSAAAAAAA AAAAAAGAG
     501 AGGAGGSYGW GDGGYGSDSA AAAAAAAAAA AGSGAGGRGD GGYGSGSSAA
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     551 AAAAAAASA ARRAGHDSA GSAAAAAAA AAAAASGAGG SGGYGWGDG
           =====
     601 GYGSDSA AAAA AAAAAG SGAGGAGGGY GWGDGGYGSD SAAAAAAA
           =====
     651 AAAASGARGS GGYGGYGSDS AAAAAAAAAA AAAGSGAGGV GGGYGWGDG
           =====
     701 YGSDSAAAAA AAAAAAGSG AGGRGDGGYG SGSSAAAAAAA AAAASAARRA
           =====
     751 GHDSAAGSAA AAAAAAAAAA ASGAGGSGGG YGWGDGGYGS DSAAAAAAA
           =====
     801 AAAAAGSGAG GAGGGYGWGD GGYGSDSA AAAA AAAA SGARGSGGYG
           =====
     851 GYGSDSA AAAA AAAAAG SGAGGVGGGY GWGDGGYGSD SAAAAAAA
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     901 AAAGSGAGGR GDGGYGS GSS AAAAAAAAAA SAARRAGHDS AAGSAAAAA
     951 AAAAAASGA GSGGGYGWG DGGYGSDSA AAAAAAAAAA AGSGAGGAGG
           =====
    1001 GYGWGDGGYG SDSAAAAAAA AAAAASGAR GSGGYGGYGS DSAAAAAAA
           =====
    1051 AAAAAGSGAG GVGGGYGWGD GGYGSDSA AAAA AAAA SGAGGRGDG
           =====
    1101 YGSGSSAAAA AAAAAAARR AGHDRAAGSA AAAAAAAAAA AASGAGSGG
    1151 GYGWGDGGYG SDSAAAAAAA AAAAAASGA GSGGYGGYG SDSAAAAAAA
           =====
    1201 AAAAAAGSGA GGAGGGYGWG DGGYGSDSA AAAAAAAAAA ASGAGGSGGY
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    1251 GGYGGYGS DS AAAAAAAAAA AAAGSGAGGA GGGYGWGDG YGSDSAAAAA
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1301 AAAAAAAGSG AGGRGDGGYG SGSSAAAAAA AAAAAARRA GHDRAGSAA
1351 AAAAAAASGAG ASGAGGSGGG YGWDGGYGGS DSAAAAAASGAG
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1401 GSGGYGGYGGS DSAAAAAASGAG AAAAAGSGAG GVGGGYGWGD GYGSDSAAA
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1451 AAAAAAASGAG SGAGGSGGYG GYGSDSAAAA AAAAAARRA SGAGGAGGYG
1501 GYGSDSAAAA AAAAAAASGAG SGAGGAGGGY GWGDGGYGGSY SAAAAAASGAG
1551 AAAGSGAGGR GDGGYGSGSS AAAAAAARRA AARRAGHDRA AGSAAAAAASGAG
1601 AAAAAASGAG GAGGGYGWGD GGYSSDSAAA AAAAAAARRA GSGAGGAGGG
1651 YGWDGDDGYGS DSAAAAAASGAG AAAAGSGAGG RGGGYGWGDG GYGSDSAAAA
=====
1701 AAAAAAASGAG GAGGRGDGGY GSGSSAAAAA AAAAAARRA GHDRAGSAA
1751 AAAAAAASGAG SGAGGSGGSY GWGDGGYGSD SAAAAAASGAGS
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1801 GGYGGYGGYG GYGSDSAAAA AAAAAAARRA AGSGAGGVGG GYGWDGGYG
=====
1851 SDSAAAAAASGAG AAAAAGSGAG GRGDGGYGSG SSAAAAAARRA AAAARRAGHD
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1901 RAAGSAAAAA AAAAAAASGAG AGGAGGGYGW GDGGYGSDSA AAAAAAARRA
=====
1951 AAGSGAGGAG GYGWGDGGY GSDSAAAAA AAAAAAGSGA GGRGGYGWGD
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2001 DGGYGSDSAA AAAAAAARRA GSGAGGRGDG GYGSGSSAAA AAAAAAARRA
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2101 AAAAAAGSGA GGAGGYGGYG GYGSDSAAAA AAAAAAARRA SGAGGVGGYG
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2151 GWGDGGYGSD SAAAAAARRA AAAAGSGAGG RGDGGYGSGS SAAAAAARRA
=====
2201 AAARRAGHER AAGSAAAAA AAAAAASGAG RSGGSYGWGD GYGSDSAAA
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2251 AAAAAAARRA SGAGGSGGYG GYGYGSDSA AAAAAAARRA ASGAGGAGGY
2301 GGYGGYGSGY SDSAAAAAARRA AAAAGSGAGG VGGYGWGDG GYGSDSAAAA
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2351 AAAAAAARRA GAGRRRGYGA YGSDSSAAAA AAAAAASGAG GSGGGYGWGD
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2401 GYGSDSAAA AAAAAAARRA AGSGAGGIGG GFGRGDGGYG SGSSAAAAA
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2451 AAAAAARRA HGRSAGSAAA AAAAAAARRA SGAGGSGGSY GWDYESYSGS
2501 SAAAAAGSGA GSGGGYGWGD DGGYGSGSSA AAAAAAARRA GSRRSGHDRA
2551 YGAGSAAAAA AAAAAAGAGAS RQVGIYGTDD GFVLDGGYDS EGSAAAAAARRA
2601 AAAAASSGR STEGHPLLSI CCRPCSHSHS YEASRISVH

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HITS AT: 257-268, 322-333, 409-420, 508-519, 595-606, 630-641,
694-705, 781-792, 816-827, 880-891, 967-978, 1002-1013,
1066-1077, 1152-1163, 1217-1228, 1284-1295, 1371-1382,
1436-1447, 1685-1696, 1770-1781, 1842-1853, 1928-1939,
1997-2008, 2150-2161, 2236-2247, 2335-2346, 2396-2407

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L2 ANSWER 17 OF 17 REGISTRY COPYRIGHT 2005 ACS on STN

RN 185261-70-5 REGISTRY

CN Fibroin (Antheraea pernyi clone pApF1.4fibroin C-terminal fragment) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN GenBank BAA11860
CN GenBank BAA11860 (Translated from: GenBank D83241)
FS PROTEIN SEQUENCE
SQL 421

SEQ 1 SGSSAAAAAA AAAASRRAGH ERAAGSAAAA AAAAAAASG VGRSGGSYGW
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51 GDGGYGSDSA AAAAAAAAAA AAASGAGGAG VCRGYGGYGS DGSGSAAAAA
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101 AAAAAAGSGA GGVGGGYGWG DGAYGSDSAA AAAAAAAAAA GSGAGGRRGY
151 GAYGSDSSAA AAAAAAASG AGGSGGGYGW GDGGYGSDSA AAAAAAAAAA
==== =====

201 AAAGSGAGGI GGGFGRGDGG YGSGSSAAAA AAAAAAARR AGHGRSAGSA
251 AAAAAAAAAA AASGAGGSGG SYGWDYESYG SGSAAAAAGS GAGGSGGGYG
301 WGDGGYGSGS SAAAAAAAAA AAGSRRSGHD RAYGAGSAAA AAAAAAGAG
351 ASRQVGIIYT DDGFILDGGY DSEGSAAAAA AAAAAAASS GRSTEGHPLL
401 SICCRPCSHS HSYEASRPV H

HITS AT: 48-59, 178-189

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> fil caplus

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<http://www.cas.org/infopolicy.html>

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L1 6 SEA FILE=REGISTRY ABB=ON PLU=ON VITTDSDGNE/SQSP

L3 4 SEA FILE=CAPLUS ABB=ON PLU=ON L1

=> d que 14

L2 17 SEA FILE=REGISTRY ABB=ON PLU=ON YGWGDGGYGS/SDS/SQSP
L4 5 SEA FILE=CAPLUS ABB=ON PLU=ON L2

=> d l3 .ca 1-4; d .ca l4 1-5

L3 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1035641 CAPLUS Full-text
DOCUMENT NUMBER: 142:33017
TITLE: Cell growth-promoting peptides from silk proteins
INVENTOR(S): Tsubouchi, Kozo; Yamada, Hiroo
PATENT ASSIGNEE(S): National Institute of Agrobiological Resources NIAR,
Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 27 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	----	-----	-----	-----
JP 2004339189	A2	20041202	JP 2003-406608	20031204
US 2005143296	A1	20050630	US 2004-789494	20040227
CN 1535723	A	20041013	CN 2004-10035241	20040301
PRIORITY APPLN. INFO.:			JP 2003-55048	A 20030228

ED Entered STN: 03 Dec 2004

AB Disclosed are cell growth-promoting peptides which comprise 4-40 amino acids from noncryst. peptide chains of the silk proteins. The peptides are obtained by hydrolyzing silk worm proteins or Antheraea cocoon fibroins and separating them by mol. weight fraction. The peptides are effective as cell growth promoters, cell adhesives, wound healing promoters, and cell culture matrixes. Also claimed is a cosmetic containing the peptides.

IC ICM C07K014-435
ICS A61K007-00; A61K038-00; A61K038-17; A61P017-02; C07K001-12;
C12N005-06; C12P021-06

CC 1-12 (Pharmacology)
Section cross-reference(s): 62, 63

IT 714954-20-8P 714954-21-9P 799804-72-1P 799804-73-2P
799804-74-3P 799804-75-4P 799804-76-5P 799804-77-6P
RL: COS (Cosmetic use); NPO (Natural product occurrence); PAC
(Pharmacological activity); PNU (Preparation, unclassified); BIOL
(Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(cell growth-promoting peptides from silk proteins)

IT 803731-18-2 803731-19-3 803731-20-6 803731-21-7 803731-22-8
803731-23-9 803731-24-0 803731-25-1 803731-26-2 803731-27-3
803731-28-4 803731-29-5 803731-30-8 803731-31-9 803731-32-0
803731-33-1 803731-34-2 803731-36-4 803731-37-5 803731-38-6
803731-39-7 803731-40-0 803731-41-1 803731-44-4 803731-46-6
803731-47-7 803731-48-8 803731-49-9 803731-50-2 803731-51-3
803731-52-4 803731-53-5 803731-54-6 803731-55-7 803731-56-8
~~803823-75-8~~ 803823-76-9 803823-77-0 803823-78-1
803823-79-2 803823-80-5 803823-81-6 803823-82-7 803823-83-8
RL: PRP (Properties)
(unclaimed sequence; cell growth-promoting peptides from silk proteins)

L3 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:838448 CAPLUS Full-text
DOCUMENT NUMBER: 141:82207
TITLE: Identification of fibroin-derived peptides enhancing

the proliferation of cultured human skin fibroblasts

AUTHOR(S): Yamada, Hiromi; Igarashi, Yumiko; Takasu, Yoko; Saito, Hitoshi; Tsubouchi, Kozo

CORPORATE SOURCE: Entomological Science, National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, 305-8634, Japan

SOURCE: Biomaterials (2003), Volume Date 2004, 25(3), 467-472
CODEN: BIMADU; ISSN: 0142-9612

PUBLISHER: Elsevier Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 27 Oct 2003

AB The authors previously reported that the fibroin of the silkworm *Bombyx mori* enhanced the proliferation of cultured human skin fibroblasts. In this work, the fibroin was digested by chymotrypsin, and the resulting peptide fragments were fractionated and assayed for their biol. activity. Two peptides that promoted fibroblast growth were isolated and identified to be VITDSDGNE and NINDFDED. Both sequences are found in the N-terminal region of the fibroin polypeptide and are thought to be the active principle of fibroblast growth-promoting activity.

CC 1-12 (Pharmacology)
Section cross-reference(s): 12

IT 714954-20-8 714954-21-9
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(fibroin-derived peptides enhancing proliferation of cultured human skin fibroblasts)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:593459 CAPLUS Full-text

DOCUMENT NUMBER: 139:287022

TITLE: The 62-kb upstream region of *Bombyx mori* fibroin heavy chain gene is clustered of repetitive elements and candidate matrix association regions

AUTHOR(S): Zhou, Cong-Zhao; Confalonieri, Fabrice; Esnault, Catherine; Zivanovic, Yvan; Jacquet, Michel; Janin, Joel; Perasso, Roland; Li, Zhen-Gang; Duguet, Michel

CORPORATE SOURCE: Institut de Genetique et Microbiologie, Universite Paris-Sud et CNRS, Orsay, 91405, Fr.

SOURCE: Gene (2003), 312, 189-195
CODEN: GENED6; ISSN: 0378-1119

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 04 Aug 2003

AB We sequenced an 80 kb DNA region containing the complete sequence of the silkworm *Bombyx mori* fibroin gene and its flanking, especially the upstream, regions (.apprx.62 kb). About 30% of the 62 kb upstream region is composed of repetitive elements including short interspersed elements Bm1, long interspersed elements L1Bm and mariner-like elements Bmmar1 which are widespread over the silkworm genome. This 62 kb region is also enriched of commonly considered matrix association region (MAR) motifs. A total of 25 individual MAR recognition signatures (MRSs) were identified, with 24 at the upstream and one at the downstream region. Combining two newly developed MAR prediction programs (MAR-finder and Chrclass), ten candidate MARs were predicted, with five containing MRS and seven related to the repetitive elements. The wide distribution of nested repetitive elements, candidate MARs, DNase I hypersensitive sites and other potential regulatory factors

recognition sites indicates this region is probably a unique huge cis-acting element contributing to the regulation of the spatial and temporal specificity and efficiency of fibroin gene expression.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 6, 12

IT 303229-60-9, Fibroin heavy chain (silkworm strain p50)

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; 62-kb upstream region of Bombyx mori fibroin heavy chain gene has clustered repetitive elements and candidate matrix association regions)

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:472155 CAPLUS Full-text

DOCUMENT NUMBER: 133:330213

TITLE: Fine organization of Bombyx mori fibroin heavy chain gene

AUTHOR(S): Zhou, Cong-Zhao; Confalonieri, Fabrice; Medina, Nadine; Zivanovic, Yvan; Esnault, Catherine; Yang, Tie; Jacquet, Michel; Janin, Joel; Duguet, Michel; Perasso, Roland; Li, Zhen-Gang

CORPORATE SOURCE: Institut de Genetique et Microbiologie and Laboratoire de Biologie Cellulaire 4, Universite Paris-Sud et CNRS, Orsay, 91405, Fr.

SOURCE: Nucleic Acids Research (2000), 28(12), 2413-2419
CODEN: NARHAD; ISSN: 0305-1048

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 13 Jul 2000

AB The complete sequence of the Bombyx mori fibroin gene has been determined by means of combining a shotgun sequencing strategy with phys. map-based sequencing procedures. It consists of two exons (67 and 15 750 bp, resp.) and one intron (971 bp). The fibroin coding sequence presents a spectacular organization, with a highly repetitive and G-rich (.apprx.45%) core flanked by non-repetitive 5' and 3' ends. This repetitive core is composed of alternate arrays of 12 repetitive and 11 amorphous domains. The sequences of the amorphous domains are evolutionarily conserved and the repetitive domains differ from each other in length by a variety of tandem repeats of subdomains of .apprx.208 bp which are reminiscent of the repetitive nucleosome organization. A typical composition of a subdomain is a cluster of repetitive units, Ua, followed by a cluster of units, Ub, (with a Ua:Ub ratio of 2:1) flanked by conserved boundary elements at the 3' end. Moreover some repeats are also perfectly conserved at the peptide level indicating that the evolutionary pressure is not identical along the sequence. A tentative model for the constitution and evolution of this unusual gene is discussed.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 12

IT 303229-60-9

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; fine organization of Bombyx mori fibroin heavy chain gene)

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 2004:1035641 CAPLUS Full-text
 DOCUMENT NUMBER: 142:33017
 TITLE: Cell growth-promoting peptides from silk proteins
 INVENTOR(S): Tsubouchi, Kozo; Yamada, Hiroo
 PATENT ASSIGNEE(S): National Institute of Agrobiological Resources NIAR,
 Japan
 SOURCE: Jpn. Kokai Tokkyo Koho, 27 pp.
 CODEN: JKXXAF
 DOCUMENT TYPE: Patent
 LANGUAGE: Japanese
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2004339189	A2	20041202	JP 2003-406608	20031204
US 2005143296	A1	20050630	US 2004-789494	20040227
CN 1535723	A	20041013	CN 2004-10035241	20040301
PRIORITY APPLN. INFO.:			JP 2003-55048	A 20030228

ED Entered STN: 03 Dec 2004

AB Disclosed are cell growth-promoting peptides which comprise 4-40 amino acids from noncryst. peptide chains of the silk proteins. The peptides are obtained by hydrolyzing silk worm proteins or Antheraea cocoon fibroins and separating them by mol. weight fraction. The peptides are effective as cell growth promoters, cell adhesives, wound healing promoters, and cell culture matrixes. Also claimed is a cosmetic containing the peptides.

IC ICM C07K014-435
 ICS A61K007-00; A61K038-00; A61K038-17; A61P017-02; C07K001-12;
 C12N005-06; C12P021-06

CC 1-12 (Pharmacology)
 Section cross-reference(s): 62, 63

IT 714954-20-8P 714954-21-9P 799804-72-1P 799804-73-2P
~~799804-74-3P~~ 799804-75-4P 799804-76-5P 799804-77-6P
 RL: COS (Cosmetic use); NPO (Natural product occurrence); PAC
 (Pharmacological activity); PNU (Preparation, unclassified); BIOL
 (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
 (cell growth-promoting peptides from silk proteins)

IT 803731-18-2 803731-19-3 803731-20-6 803731-21-7 803731-22-8
 803731-23-9 803731-24-0 803731-25-1 803731-26-2 ~~803731-27-3~~
 803731-28-4 ~~803731-29-5~~ 803731-30-8 ~~803731-31-9~~
 803731-32-0 ~~803731-33-1~~ ~~803731-34-2~~ 803731-36-4
 803731-37-5 ~~803731-38-6~~ 803731-39-7 ~~803731-40-0~~
 803731-41-1 ~~803731-44-4~~ 803731-46-6 803731-47-7
 803731-48-8 803731-49-9 803731-50-2 803731-51-3 803731-52-4
 803731-53-5 ~~803731-54-6~~ 803731-55-7 803731-56-8
 803823-75-8 803823-76-9 803823-77-0 ~~803823-78-1~~
 803823-79-2 803823-80-5 803823-81-6 803823-82-7 803823-83-8
 RL: PRP (Properties)
 (unclaimed sequence; cell growth-promoting peptides from silk proteins)

L4 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 2003:997528 CAPLUS Full-text
 DOCUMENT NUMBER: 140:195109
 TITLE: Variation and characterization analysis of partial
 fragment of fibroin gene from silkworm, Antheraea
 pernyi
 AUTHOR(S): Li, Wenli; Jin, Liji; An, Lija
 CORPORATE SOURCE: Department of Bioengineering Chemistry, Dalian

University of Technology, Dalian, 116023, Peop. Rep.
China

SOURCE: High Technology Letters (2003), 9(3), 29-32

CODEN: HTLEFC; ISSN: 1006-6748

PUBLISHER: High Technology Letters Press

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 23 Dec 2003

AB A 1.4Kb DNA fragment containing 3' flanking sequence of fibroin gene of silkworm, *Antheraea pernyi*, was obtained from the silk gland's mRNA of 5th larva. Anal. of this sequence with another *A. pernyi* fibroin protein (accession Number D83241) revealed that it consists of a completely open reading frame (ORF), which includes 14 polyalanine-containing units (motifs) and 100bp 3'-UTR. The sequence of the predicted amino acid reveals the highest level of overall identity (90%) with D83241. It was found that it loses a repeat region at the upstream of TAA codon and some mutations. A putative polyadenylation signal AATAAA tail was found in position 1300, which follows the termination codon.

CC 6-3 (General Biochemistry)

Section cross-reference(s): 3, 11

IT 663232-47-1

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; partial sequence and conserved protein motifs of
fibroin from silkworm (*Antheraea pernyi*))

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:669212 CAPLUS Full-text

DOCUMENT NUMBER: 136:242651

TITLE: Cloning of the fibroin gene from the oak silkworm,
Antheraea yamamai and its complete sequence

AUTHOR(S): Hwang, Jae-Sam; Lee, Jin-Sung; Goo, Tae-Won; Yun,
Eun-Young; Lee, Kwang-Sik; Kim, Yong-Sung; Jin,
Byung-Rae; Lee, Sang-Mong; Kim, Keun-Young; Kang,
Seok-Woo; Suh, Dong-Sang

CORPORATE SOURCE: Department of Sericulture and Entomology, National
Institute of Agricultural Science and Technology, RDA,
Suwon, 441-100, S. Korea

SOURCE: Biotechnology Letters (2001), 23(16), 1321-1326

CODEN: BILED3; ISSN: 0141-5492

PUBLISHER: Kluwer Academic Publishers

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 13 Sep 2001

AB The nucleotide sequences containing an entire genomic region and 5' upstream region of *Antheraea yamamai* fibroin gene have been determined. The gene consists of an initial exon encoding 14 amino acids, an intron (150 bp), and a long second exon coding for 2641 amino acids. The fibroin coding sequence shows a specialized organization with a highly repetitive region flanked by non repetitive 5' and 3' ends. Northern blot analyses confirmed that fibroin gene is actively expressed in the posterior silk gland of the final instar larvae of *Antheraea yamamai*.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 6, 12

IT 404318-03-2, Fibroin (*Antheraea yamamai*)

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; sequence of the fibroin gene from the oak

silkworm, *Antheraea yamamai*)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:831431 CAPLUS Full-text

DOCUMENT NUMBER: 134:362047

TITLE: Dynamic rearrangement within the *Antheraea pernyi* silk
fibroin gene is associated with four types of
repetitive units

AUTHOR(S): Sezutsu, Hideki; Yukuhiro, Kenji

CORPORATE SOURCE: Department of Insect Genetic Breeding, National
Institute of Sericultural and Entomological Science,
Tsukuba, 305-8634, Japan

SOURCE: Journal of Molecular Evolution (2000), 51(4), 329-338
CODEN: JMEVAU; ISSN: 0022-2844

PUBLISHER: Springer-Verlag New York Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 29 Nov 2000

AB We characterized a full-length gene encoding wild silkworm *Antheraea pernyi*
fibroin (Ap-fibroin) to clarify the conformation of repetitive sequences. The
gene consisted of a first exon encoding 14 amino acid residues, a short intron
(120 bp), and a long second exon encoding 2,625 amino acid residues. Three
amino acids, alanine, glycine, and serine, amounted to 81% of the Ap-fibroin
sequence. The Ap-fibroin, except for 155 residues of the amino terminus, was
composed of 80 tandemly arranged polyalanine-containing units (motifs). A
motif was a doublet of a polyalanine block (PAB) and a nonpolyalanine block
(NPAB). Seventy-eight of the 80 motifs were classified into four types based
on differences in the NPAB sequences. Although resp. motifs were
significantly conserved, many rearrangements were observed within the second
exon, i.e., the triplication of a 558-bp-long sequence and other duplication
events of shorter sequences. Chi-like sequences, GCTGGAG, might contribute to
the rearrangement within the gene as described in human minisatellite loci,
because they were found at specific sites of NPAB-encoding sequences in three
of four types of motifs. The present results support the idea that the Ap-
fibroin gene is unstable like minisatellite sequences and that the evolution
of this gene is strongly associated with its instability.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 6, 12

IT 336885-96-2, Fibroin (*Antheraea pernyi* clone AP2)

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; dynamic rearrangement within the *Antheraea pernyi*
silk fibroin gene is associated with four types of repetitive units)

REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1997:15804 CAPLUS Full-text

DOCUMENT NUMBER: 126:55749

TITLE: Preferential codon usage and two types of repetitive
motifs in the fibroin gene of the Chinese oak
silkworm, *Antheraea pernyi*

AUTHOR(S): Yukuhiro, K.; Kanda, T.; Tamura, T.

CORPORATE SOURCE: Inst. Sericultural Entomological Science, Ministry
Agriculture Fisheries and Forestry, Ibaraki, 305,
Japan

SOURCE: Insect Molecular Biology (1997), 6(1), 89-95
CODEN: IMBIE3; ISSN: 0962-1075

PUBLISHER: Blackwell
DOCUMENT TYPE: Journal
LANGUAGE: English

ED Entered STN: 11 Jan 1997

AB In this paper we describe the peculiar structures and preferential codon usage found in wild silkworm fibroin genes. We determined a 1350 bp nucleotide sequence from the Chinese oak silkworm, *Antheraea pernyi*. The deduced amino acid sequence was partitioned into thirteen polyalanine-containing repetitive motifs, which was one of the characteristic of *Antheraea* fibroins. Eleven of these arrays can be classified into two types of motifs depending on difference in amino acid sequences following polyalanine. Repetitive motifs structurally similar to those of *A. pernyi* were detected in a homolog of the Japanese oak silkworm, *Antheraea yamamai*. The most remarkable feature of this study was preferential codon usage, especially seen in alanine synonymous codons within both homologs of *Antheraea*: isocodon GCA most frequently occurred in alanine isocodons. In contrast, GCU isocodon was the most abundant in *Bombyx mori* fibroin heavy chain that lacks polyalanine arrays. This result strongly suggests different modes of selective constraint between the two types of fibroin gene. The similar finding that GCA isocodon was most frequent in two dragline silk sequences of the spider, *Nephila clavipes*, is consistent with our results because of the repetitive polyalanine-containing arrays seen in spider dragline silk.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 6, 12

IT 185261-70-5

RL: PRP (Properties)

(amino acid sequence; preferential codon usage and two types of repetitive motifs in the fibroin gene of the Chinese oak silkworm, *Antheraea pernyi*)

REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2005, 08:04:00 ; Search time 132.727 Seconds
(without alignments)
53.156 Million cell updates/sec

Title: US-10-789-494B-1
Perfect score: 51
Sequence: 1 VITDSDGNE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	51	100.0	178	1 FIBH_BOMMA	Q99050 bombyx mand
2	51	100.0	5263	1 FIBH_BOMMO	P05790 bombyx mori
3	43	84.3	317	2 Q9VIX8_DROME	Q9vix8 drosophila
4	42	82.4	907	2 Q733M3_BACC1	Q733m3 bacillus ce
5	42	82.4	11103	2 Q54CU4_DICDI	Q54cu4 dictyosteli
6	41	80.4	150	2 Q742N8_MYCPA	Q742n8 mycobacteri
7	41	80.4	361	2 Q8X078_NEUCR	Q8x078 neurospora
8	40	78.4	318	1 CYPR_YEAST	P25334 saccharomyc
9	40	78.4	423	2 Q4IDY7_GIBZE	Q4idy7 gibberella
10	40	78.4	1312	2 Q9U113_LEIMA	Q9ul13 leishmania
11	40	78.4	1326	2 Q6FR84_CANGA	Q6fr84 candida gla
12	40	78.4	1597	2 Q6BXP0_DEBHA	Q6bxp0 debaryomyce
13	39	76.5	121	2 Q6Q4F2_ACTAC	Q6q4f2 actinobacil
14	39	76.5	336	2 Q7T6X9_MIMIV	Q7t6x9 mimivirus.
15	39	76.5	359	2 Q84V38_VITVI	Q84v38 vitis vinif

16	39	76.5	467	2	Q53XD3_DROME	Q53xd3	drosophila
17	39	76.5	475	1	IF2G_DROME	Q24208	drosophila
18	39	76.5	559	1	MDL1_PRUDU	O24243	prunus dulc
19	39	76.5	559	2	Q7XJE8_PRUDU	Q7xje8	prunus dulc
20	39	76.5	563	2	Q7PL55_DROME	Q7pl55	drosophila
21	39	76.5	744	2	Q7PL56_DROME	Q7pl56	drosophila
22	39	76.5	907	2	Q4MNH3_BACCE	Q4mnh3	bacillus ce
23	39	76.5	907	2	Q81AF6_BACCR	Q81af6	bacillus ce
24	39	76.5	907	2	Q6HFI4_BACHK	Q6hfi4	bacillus th
25	39	76.5	907	2	Q637L2_BACCZ	Q637l2	bacillus ce
26	39	76.5	907	2	Q81Y80_BACAN	Q81y80	debacillus an
27	39	76.5	1257	2	Q6BVF7_DEBHA	Q6bvf7	debaryomyce
28	39	76.5	1511	2	Q8A0B0_BACTN	Q8a0b0	bacteroides
29	39	76.5	2233	2	Q81890_PI3B	Q81890	bovine para
30	38	74.5	237	1	LECA_DIOGU	P81637	dioclea gui
31	38	74.5	244	2	Q8K8B0_STRP3	Q8k8b0	streptococc
32	38	74.5	244	2	Q9A100_STRPY	Q9a100	streptococc
33	38	74.5	244	2	Q8P215_STRP8	Q8p215	streptococc
34	38	74.5	252	2	Q878E9_STRP3	Q878e9	streptococc
35	38	74.5	252	2	Q5XDA1_STRP6	Q5xda1	streptococc
36	38	74.5	257	2	Q8UFQ2_AGRT5	Q8ufq2	agrobacteri
37	38	74.5	296	2	Q9NF63_CAEEL	Q9nf63	caenorhabdi
38	38	74.5	328	2	Q6GUL4_9BACT	Q6gul4	prevotella
39	38	74.5	367	2	Q9HMM3_HALSA	Q9hmm3	halobacteri
40	38	74.5	373	2	Q6VSY7_9VIRU	Q6vsy7	vibrio para
41	38	74.5	383	2	Q5MK34_9PAST	Q5mk34	pasteurella
42	38	74.5	391	2	Q5MK37_9PAST	Q5mk37	pasteurella
43	38	74.5	392	2	Q5MK35_9PAST	Q5mk35	pasteurella
44	38	74.5	394	2	Q5MK32_9PAST	Q5mk32	pasteurella
45	38	74.5	437	2	Q22993_CAEEL	Q22993	caenorhabdi
46	38	74.5	510	2	Q5B4P9_EMENI	Q5b4p9	aspergillus
47	38	74.5	550	1	PME22_LYCES	Q96575	lycopersico
48	38	74.5	593	2	Q6A5C6_PROAC	Q6a5c6	propionibac
49	38	74.5	683	1	YPR4_CAEEL	Q20059	caenorhabdi
50	38	74.5	782	2	Q93SH4_BRAJA	Q93sh4	bradyrhizob
51	38	74.5	788	2	Q89EK1_BRAJA	Q89ek1	bradyrhizob
52	38	74.5	917	2	Q88UJ0_LACPL	Q88uj0	lactobacill
53	38	74.5	953	1	LKA11_PASHA	P55118	pasteurella
54	38	74.5	953	1	LKA1A_PASHA	P16535	pasteurella
55	38	74.5	953	1	LKA1B_PASHA	Q7bhi8	pasteurella
56	38	74.5	953	1	LKA2D_PASHA	Q9ev29	pasteurella
57	38	74.5	953	1	LKA7A_PASHA	P0c084	pasteurella
58	38	74.5	953	1	LKTA6_PASHA	P0c083	pasteurella
59	38	74.5	953	1	LKTA8_PASHA	Q9ev34	pasteurella
60	38	74.5	953	1	LKTA_MANGL	Q9etx2	mannheimia
61	38	74.5	953	2	Q6TB03_9PAST	Q6tb03	mannheimia
62	38	74.5	1012	1	UBA1_SCHPO	O94609	schizosacch
63	38	74.5	3444	2	Q4Q439_LEIMA	Q4q439	leishmania
64	37	72.5	127	2	Q8C3K4_MOUSE	Q8c3k4	mus musculu
65	37	72.5	147	2	Q6ENJ8_ORYSA	Q6enj8	oryza sativ
66	37	72.5	169	2	Q5FGQ4_EHRRG	Q5fgq4	ehrlichia r
67	37	72.5	177	2	Q6VCX3_EHRRU	Q6vcx3	ehrlichia r
68	37	72.5	177	2	Q5HA06_EHRRW	Q5ha06	ehrlichia r
69	37	72.5	242	2	Q22207_CAEEL	Q22207	caenorhabdi
70	37	72.5	349	2	Q22512_CAEEL	Q22512	caenorhabdi
71	37	72.5	507	1	FRS2_MOUSE	Q8c180	mus musculu
72	37	72.5	509	2	Q8UVU3_XENLA	Q8uvu3	xenopus lae

73	37	72.5	509	2	Q90ZF5_XENLA	Q90zf5 xenopus lae
74	37	72.5	509	2	Q7ZWM2_XENLA	Q7zwm2 xenopus lae
75	37	72.5	511	1	FRS2_HUMAN	Q8wu20 homo sapien
76	37	72.5	580	2	Q4H4Q5_9DEIO	Q4h4q5 deinococcus
77	37	72.5	585	2	Q6QPZ0_9LACT	Q6qpz0 lactococcus
78	37	72.5	604	2	Q50SY3_ENTHI	Q50sy3 entamoeba h
79	37	72.5	814	2	Q648S9_9ARCH	Q648s9 uncultured
80	37	72.5	817	2	Q6ZPN1_MOUSE	Q6zpn1 mus musculu
81	37	72.5	826	2	Q8IY15_HUMAN	Q8iy15 homo sapien
82	37	72.5	862	2	Q8NTA1_CORGL	Q8nta1 corynebacte
83	37	72.5	1019	2	Q7UWL9_RHOBA	Q7uwl9 rhodopirell
84	37	72.5	1727	2	Q68FD9_MOUSE	Q68fd9 mus musculu
85	37	72.5	1865	2	Q9HCM3_HUMAN	Q9hcm3 homo sapien
86	37	72.5	1902	2	Q9AIQ2_LACLC	Q9aiq2 lactococcus
87	37	72.5	2630	2	Q6ALE1_DESPS	Q6ale1 desulfotale
88	37	72.5	4190	2	Q6K796_ORYSA	Q6k796 oryza sativ
89	36	70.6	103	2	Q595F8_MYCGA	Q595f8 mycoplasma
90	36	70.6	103	2	Q595G2_MYCGA	Q595g2 mycoplasma
91	36	70.6	103	2	Q595J5_MYCGA	Q595j5 mycoplasma
92	36	70.6	103	2	Q595J9_MYCGA	Q595j9 mycoplasma
93	36	70.6	103	2	Q595L9_MYCGA	Q595l9 mycoplasma
94	36	70.6	103	2	Q595M4_MYCGA	Q595m4 mycoplasma
95	36	70.6	103	2	Q595M6_MYCGA	Q595m6 mycoplasma
96	36	70.6	110	2	Q4LDH1_MYCGA	Q4ldh1 mycoplasma
97	36	70.6	157	2	Q7NFK5_GLOVI	Q7nfk5 gloeobacter
98	36	70.6	183	2	O10618_9NUCL	O10618 helicoverpa
99	36	70.6	201	2	Q91BY7_9NUCL	Q91by7 helicoverpa
100	36	70.6	203	2	Q77LZ1_9NUCL	Q77lz1 helicoverpa

ALIGNMENTS

RESULT 1

FIBH_BOMMA

ID FIBH_BOMMA STANDARD; PRT; 178 AA.

AC Q99050;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Fibroin heavy chain precursor (Fib-H) (H-fibroin) (Fragment).

GN Name=FIBH;

OS Bombyx mandarina (Wild silk moth) (Wild silkworm).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;

OC Bombycidae; Bombyx.

OX NCBI_TaxID=7092;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Posterior silk gland;

RA Kusuda J., Tazima Y., Onimaru K., Ninaki O., Suzuki Y.;

RT "The sequence around the 5' end of the fibroin gene from the wild

RT silkworm, Bombyx mandarina, and comparison with that of the

RT domesticated species, B. mori.";

RL Mol. Gen. Genet. 203:359-364(1986).

CC -!- FUNCTION: Core component of the silk filament; a strong, insoluble
CC and chemically inert fiber.

```

CC  -!- SUBUNIT: Silk fibroin elementary unit consists in a disulfide-
CC      linked heavy and light chain and a p25 glycoprotein in molar
CC      ratios of 6:6:1. This results in a complex of approximately 2.3
CC      MDa.
CC  -!- TISSUE SPECIFICITY: Produced exclusively in the posterior (PSG)
CC      section of silk glands, which are essentially modified salivary
CC      glands.
CC  -!- DOMAIN: Composed of antiparallel beta sheets. The strands of the
CC      beta sheets run parallel to the fiber axis. Long stretches of silk
CC      fibroin are composed of microcrystalline arrays of (-Gly-Ser-Gly-
CC      Ala-Gly-Ala-)n interrupted by regions containing bulkier residues.
CC      The fiber is composed of microcrystalline arrays alternating with
CC      amorphous regions.
CC  -!- PTM: The interchain disulfide bridge is essential for the
CC      intracellular transport and secretion of fibroin.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; X03973; CAA27612.1; -; Genomic_DNA.
KW  Repeat; Signal; Silk.
FT  SIGNAL      1      21      Potential.
FT  CHAIN       22     >178     Fibroin heavy chain.
FT  REGION     149     >178     Highly repetitive.
FT  CONFLICT    10      10      C -> V (in Ref. 1; CAA27612).
FT  NON_TER    178     178
SQ  SEQUENCE    178 AA;  18326 MW;  8E15C7E7A9682940 CRC64;

```

```

Query Match          100.0%;  Score 51;  DB 1;  Length 178;
Best Local Similarity 100.0%;  Pred. No. 0.24;
Matches   10;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy      1 VITTDSDGNE 10
        |||||
Db      85 VITTDSDGNE 94

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Search completed: December 8, 2005, 08:15:35
Job time : 137.727 secs

OM protein - protein search, using sw model

Run on: December 8, 2005, 08:04:51 ; Search time 21.3636 Seconds
(without alignments)
45.038 Million cell updates/sec

Title: US-10-789-494B-1
Perfect score: 51
Sequence: 1 VITTDSDGNE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	40	78.4	318	1	CSBYC3	peptidylprolyl iso
2	39	76.5	475	1	S46941	translation initia
3	38	74.5	237	2	A45587	lectin - Dioclea l
4	38	74.5	257	2	AI2741	conserved hypothet
5	38	74.5	257	2	H97522	hypothetical prote
6	38	74.5	296	2	T31582	hypothetical prote
7	38	74.5	367	2	H84397	hypothetical prote
8	38	74.5	437	2	T29330	hypothetical prote
9	38	74.5	683	2	T21810	hypothetical prote
10	38	74.5	686	2	T21808	hypothetical prote
11	38	74.5	953	1	B30169	leukotoxin A - Pas
12	38	74.5	1011	2	T50344	poly(A)+ RNA trans
13	38	74.5	1012	2	T52000	poly(A)+ RNA trans

14	37	72.5	242	2	T16804	hypothetical prote
15	37	72.5	349	2	T16882	hypothetical prote
16	36	70.6	455	1	A69753	glucarate dehydrat
17	36	70.6	1122	2	T18346	MGC1 protein precu
18	36	70.6	1409	2	S74916	alkaline phosphata
19	36	70.6	1481	2	S28669	pullulanase (EC 3.
20	36	70.6	1816	2	F83901	hypothetical prote
21	35	68.6	161	2	S67178	translation initia
22	35	68.6	311	2	T24947	hypothetical prote
23	35	68.6	392	2	AD2360	hypothetical prote
24	35	68.6	409	2	T25935	hypothetical prote
25	35	68.6	415	2	S37340	flo protein homolo
26	35	68.6	491	2	T30590	alkylhalidase homo
27	35	68.6	546	2	S46527	pectinesterase (EC
28	35	68.6	914	2	S48333	ORC1 protein - yea
29	35	68.6	2174	2	E95965	hypothetical glyci
30	35	68.6	2468	2	A83412	hypothetical prote
31	35	68.6	6642	2	T29757	protein UNC-89 - C
32	35	68.6	13055	2	T16580	hypothetical prote
33	34	66.7	88	2	S31030	gene 85 protein -
34	34	66.7	170	2	A97964	conserved hypothet
35	34	66.7	217	2	AI0987	probable lipoprote
36	34	66.7	228	2	G70532	hypothetical prote
37	34	66.7	273	2	T34234	hypothetical prote
38	34	66.7	275	2	D96926	prephenate dehydro
39	34	66.7	299	2	E82116	flagellar biosynth
40	34	66.7	353	2	T35221	probable ATP/GTP b
41	34	66.7	374	2	T46065	hypothetical prote
42	34	66.7	379	2	H70102	hypothetical prote
43	34	66.7	407	2	AF2497	transposase all715
44	34	66.7	424	2	T43498	hypothetical prote
45	34	66.7	443	2	D82975	two-component sens
46	34	66.7	544	2	T07593	pectinesterase (EC
47	34	66.7	550	2	S46528	pectinesterase (EC
48	34	66.7	630	2	T00352	hypothetical prote
49	34	66.7	678	2	T50256	probable vacuolar
50	34	66.7	686	2	A55665	microtubule-associ
51	34	66.7	813	2	G83662	class III stress r
52	34	66.7	1160	2	A46423	transcription fact
53	34	66.7	1176	2	T47444	hypothetical prote
54	34	66.7	1441	2	T39636	probable cleavage
55	34	66.7	2233	1	ZLNZP3	genome polyprotein
56	34	66.7	2340	2	B71704	cell surface antig
57	34	66.7	3643	2	T36410	probable polyketid
58	33	64.7	75	2	T12210	endopeptidase Clp
59	33	64.7	124	2	T24876	hypothetical prote
60	33	64.7	146	2	A69950	conserved hypothet
61	33	64.7	165	2	T26885	hypothetical prote
62	33	64.7	185	2	H82799	fimbrillin XF0487
63	33	64.7	194	2	E86885	hypothetical prote
64	33	64.7	219	2	AF0639	flagellar basal bo
65	33	64.7	237	2	JU0176	lectin alpha chain
66	33	64.7	280	2	S35103	bone sialoprotein
67	33	64.7	289	2	A89865	hypothetical prote
68	33	64.7	315	2	G91004	hypothetical prote
69	33	64.7	315	2	A85849	unknown protein en
70	33	64.7	341	2	E71564	probable cationic

71	33	64.7	356	2	F84072	hypothetical prote
72	33	64.7	366	2	E59102	hypothetical prote
73	33	64.7	378	1	QXBY33	oxi3 intron 3 prot
74	33	64.7	451	2	A86470	protein F21H2.12 [
75	33	64.7	463	2	T14884	hypothetical prote
76	33	64.7	466	2	E70865	trigger factor tig
77	33	64.7	469	2	B87094	probable molecular
78	33	64.7	513	2	S38197	sucrose transport
79	33	64.7	585	2	C70330	conserved hypothet
80	33	64.7	627	2	A41609	dnaK-type molecula
81	33	64.7	656	2	D96831	hypothetical prote
82	33	64.7	698	2	S52674	general sporulatio
83	33	64.7	730	2	AI3480	penicillin-binding
84	33	64.7	812	1	MMECOF	outer membrane ush
85	33	64.7	843	2	S33442	EF protein - Strep
86	33	64.7	923	1	B35905	endopeptidase Clp
87	33	64.7	926	1	A35905	endopeptidase Clp
88	33	64.7	967	2	S66852	hypothetical prote
89	33	64.7	995	2	S50358	hypothetical prote
90	33	64.7	1137	2	G70868	probable regulator
91	33	64.7	1272	2	T30248	fragile X mental r
92	33	64.7	1475	2	A44765	alpha-amylase (EC
93	33	64.7	1822	2	S33441	EF protein - Strep
94	33	64.7	1879	2	T19481	hypothetical prote
95	33	64.7	1902	2	S06997	lactocepin (EC 3.4
96	33	64.7	1902	2	B45764	lactocepin (EC 3.4
97	33	64.7	3013	2	AB0480	probable invasin Y
98	33	64.7	3283	2	AC1018	large repetitive p
99	33	64.7	4447	2	A69679	polyketide synthas
100	33	64.7	4558	2	C82199	RTX toxin RtxA VC1

ALIGNMENTS

RESULT 1

CSBYC3

peptidylprolyl isomerase (EC 5.2.1.8) SCC3 precursor - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: cyclophilin SCC3; PPIase SCC3; protein YCR069w; protein YCR070w

C;Species: *Saccharomyces cerevisiae*

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C;Accession: S26658; S26587; S19484; S19517

R;Franco, L.; Jimenez, A.; Demolder, J.; Molemans, F.; Fiers, W.; Contreras, R. Yeast 7, 971-979, 1991

A;Title: The nucleotide sequence of a third cyclophilin-homologous gene from *Saccharomyces cerevisiae*.

A;Reference number: S26658; MUID:92206076; PMID:1803821

A;Accession: S26658

A;Molecule type: DNA

A;Residues: 1-318 <FRA>

A;Cross-references: UNIPROT:P25334; UNIPARC:UPI0000128C9D

R;Ballesta, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.; Remacha, M.; Sanz, E. submitted to the Protein Sequence Database, October 1992

A;Reference number: S26587

A;Accession: S26587

A;Molecule type: DNA
 A;Residues: 1-318 <BAL1>
 A;Cross-references: UNIPARC:UPI0000128C9D; EMBL:X59720; NID:g1907116;
 PIDN:CAA42275.1; PID:g1907209; GSPDB:GN00003; MIPS:YCR069w
 A;Note: this is a revision to the sequence in reference S19482 and S19486
 R;Contreras, R.; Demolder, J.; Fiers, W.; Molemans, F.
 submitted to the Protein Sequence Database, March 1992
 A;Reference number: S19482
 A;Accession: S19484
 A;Molecule type: DNA
 A;Residues: 1-170 <CON>
 A;Cross-references: UNIPARC:UPI000017304A; EMBL:X59720; GSPDB:GN00003;
 MIPS:YCR069w
 A;Note: this sequence has been revised in reference S26587, resulting in
 extension of the reading frame
 R;Ballesta, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.; Remacha, M.; Sanz, E.
 submitted to the Protein Sequence Database, March 1992
 A;Reference number: S19486
 A;Accession: S19517
 A;Molecule type: DNA
 A;Residues: 'MTGLKDSQWPILDILTPRN',165-318 <BAL2>
 A;Cross-references: UNIPARC:UPI000017304B; EMBL:X59720
 A;Note: this was assumed to be protein YCR070w; the difference at the amino end
 is due to a frameshift error
 A;Note: this sequence has been revised in reference S26587
 C;Genetics:
 A;Gene: SGD:SCC3; MIPS:YCR069w
 A;Cross-references: MIPS:YCR069w; SGD:S0000665
 A;Map position: 3R
 C;Function:
 A;Description: catalyzes the cis-trans isomerization of peptidylproline peptide
 bonds
 C;Superfamily: peptidylprolyl isomerase SCC3; cyclophilin homology
 C;Keywords: cis-trans-isomerase; glycoprotein; transmembrane protein
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-318/Product: peptidylprolyl isomerase SCC3 #status predicted <MAT>
 F;51-279/Domain: cyclophilin homology <CYP>
 F;286-303/Domain: transmembrane #status predicted <TMM>
 F;166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 78.4%; Score 40; DB 1; Length 318;
 Best Local Similarity 70.0%; Pred. No. 7.1;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VITTDSDGNE 10
 :||| :|||
 Db 171 IITTKADGNE 180

Search completed: December 8, 2005, 08:16:27
 Job time : 24.3636 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2005, 08:16:37 ; Search time 5.90909 Seconds
(without alignments)
9.451 Million cell updates/sec

Title: US-10-789-494B-1
Perfect score: 51
Sequence: 1 VITTDSDGNE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	33	64.7	359	7	US-11-055-822-842	Sequence 842, App
2	33	64.7	644	6	US-10-793-626-1436	Sequence 1436, Ap
3	33	64.7	1170	6	US-10-858-730-71	Sequence 71, Appl
4	32	62.7	378	6	US-10-467-657-5322	Sequence 5322, Ap
5	32	62.7	740	7	US-11-110-837-2	Sequence 2, Appli
6	32	62.7	740	7	US-11-110-837-4	Sequence 4, Appli
7	32	62.7	784	6	US-10-467-657-5968	Sequence 5968, Ap
8	31	60.8	399	6	US-10-467-657-7478	Sequence 7478, Ap
9	31	60.8	1730	7	US-11-192-967-4	Sequence 4, Appli

10	31	60.8	1730	7	US-11-193-715-4	Sequence 4, Appli
11	31	60.8	2004	6	US-10-467-657-84	Sequence 84, Appl
12	31	60.8	2004	6	US-10-467-657-6322	Sequence 6322, Ap
13	31	60.8	2919	6	US-10-821-234-1133	Sequence 1133, Ap
14	30	58.8	261	6	US-10-467-657-6154	Sequence 6154, Ap
15	30	58.8	269	6	US-10-467-657-7278	Sequence 7278, Ap
16	30	58.8	318	6	US-10-821-234-1590	Sequence 1590, Ap
17	30	58.8	318	7	US-11-186-284-69	Sequence 69, Appl
18	30	58.8	438	7	US-11-140-417-2	Sequence 2, Appli
19	30	58.8	630	6	US-10-467-657-7014	Sequence 7014, Ap
20	30	58.8	710	7	US-11-089-551A-33	Sequence 33, Appl
21	29	56.9	141	6	US-10-793-626-2886	Sequence 2886, Ap
22	29	56.9	141	6	US-10-793-626-3084	Sequence 3084, Ap
23	29	56.9	168	6	US-10-793-626-2430	Sequence 2430, Ap
24	29	56.9	294	6	US-10-467-657-2876	Sequence 2876, Ap
25	29	56.9	319	6	US-10-793-626-792	Sequence 792, App
26	29	56.9	319	6	US-10-793-626-2008	Sequence 2008, Ap
27	29	56.9	325	7	US-11-074-176-368	Sequence 368, App
28	29	56.9	341	6	US-10-793-626-1278	Sequence 1278, Ap
29	29	56.9	373	6	US-10-131-826A-388	Sequence 388, App
30	29	56.9	421	6	US-10-858-730-1	Sequence 1, Appli
31	29	56.9	422	6	US-10-467-657-212	Sequence 212, App
32	29	56.9	422	6	US-10-467-657-6516	Sequence 6516, Ap
33	29	56.9	441	6	US-10-510-386-162	Sequence 162, App
34	29	56.9	463	6	US-10-793-626-960	Sequence 960, App
35	29	56.9	467	6	US-10-510-386-56	Sequence 56, Appl
36	29	56.9	486	6	US-10-793-626-788	Sequence 788, App
37	29	56.9	555	7	US-11-034-569-8	Sequence 8, Appli
38	29	56.9	560	7	US-11-034-569-6	Sequence 6, Appli
39	29	56.9	749	6	US-10-793-626-138	Sequence 138, App
40	29	56.9	817	6	US-10-793-626-50	Sequence 50, Appl
41	29	56.9	817	6	US-10-793-626-1528	Sequence 1528, Ap
42	29	56.9	926	6	US-10-841-129-2	Sequence 2, Appli
43	29	56.9	2314	7	US-11-013-759-11	Sequence 11, Appl
44	28.5	55.9	251	6	US-10-821-234-898	Sequence 898, App
45	28	54.9	96	7	US-11-084-554-217	Sequence 217, App
46	28	54.9	153	6	US-10-467-657-4546	Sequence 4546, Ap
47	28	54.9	193	6	US-10-467-657-2464	Sequence 2464, Ap
48	28	54.9	226	6	US-10-467-657-740	Sequence 740, App
49	28	54.9	312	7	US-11-055-822-34	Sequence 34, Appl
50	28	54.9	344	7	US-11-055-822-516	Sequence 516, App
51	28	54.9	403	6	US-10-528-031-7	Sequence 7, Appli
52	28	54.9	409	6	US-10-821-234-892	Sequence 892, App
53	28	54.9	419	7	US-11-084-624-18	Sequence 18, Appl
54	28	54.9	421	6	US-10-067-974-2	Sequence 2, Appli
55	28	54.9	421	6	US-10-067-974-16	Sequence 16, Appl
56	28	54.9	421	6	US-10-858-730-202	Sequence 202, App
57	28	54.9	421	6	US-10-525-710-73	Sequence 73, Appl
58	28	54.9	421	7	US-11-055-822-26	Sequence 26, Appl
59	28	54.9	452	7	US-11-074-176-274	Sequence 274, App
60	28	54.9	492	6	US-10-821-234-1108	Sequence 1108, Ap
61	28	54.9	496	6	US-10-485-517-324	Sequence 324, App
62	28	54.9	496	6	US-10-485-517-325	Sequence 325, App
63	28	54.9	578	6	US-10-821-234-1039	Sequence 1039, Ap
64	28	54.9	687	7	US-11-074-176-260	Sequence 260, App
65	28	54.9	741	6	US-10-467-657-6266	Sequence 6266, Ap
66	28	54.9	815	7	US-11-073-112-3	Sequence 3, Appli

67	28	54.9	890	7	US-11-106-623-28	Sequence 28, Appl
68	28	54.9	950	6	US-10-467-657-854	Sequence 854, App
69	28	54.9	1058	6	US-10-821-234-1473	Sequence 1473, Ap
70	28	54.9	1058	6	US-10-878-556A-63	Sequence 63, Appl
71	28	54.9	1058	7	US-11-069-642-105	Sequence 105, App
72	28	54.9	1377	6	US-10-467-657-7922	Sequence 7922, Ap
73	28	54.9	1394	6	US-10-467-657-7930	Sequence 7930, Ap
74	28	54.9	2376	7	US-11-096-051-4	Sequence 4, Appli
75	28	54.9	2657	6	US-10-821-234-1262	Sequence 1262, Ap
76	28	54.9	2715	7	US-11-096-051-2	Sequence 2, Appli
77	28	54.9	2715	7	US-11-113-424-51	Sequence 51, Appl
78	28	54.9	2721	7	US-11-096-051-10	Sequence 10, Appl
79	28	54.9	2725	7	US-11-096-051-8	Sequence 8, Appli
80	27	52.9	46	6	US-10-467-657-8850	Sequence 8850, Ap
81	27	52.9	123	7	US-11-076-713-3	Sequence 3, Appli
82	27	52.9	123	7	US-11-076-713-6	Sequence 6, Appli
83	27	52.9	154	6	US-10-467-657-158	Sequence 158, App
84	27	52.9	154	6	US-10-467-657-6520	Sequence 6520, Ap
85	27	52.9	154	6	US-10-467-657-7634	Sequence 7634, Ap
86	27	52.9	171	7	US-11-055-822-352	Sequence 352, App
87	27	52.9	179	6	US-10-793-626-1738	Sequence 1738, Ap
88	27	52.9	187	6	US-10-467-657-1636	Sequence 1636, Ap
89	27	52.9	198	6	US-10-467-657-4664	Sequence 4664, Ap
90	27	52.9	201	6	US-10-467-657-2006	Sequence 2006, Ap
91	27	52.9	227	6	US-10-467-657-2624	Sequence 2624, Ap
92	27	52.9	304	6	US-10-467-657-7410	Sequence 7410, Ap
93	27	52.9	320	7	US-11-000-463-354	Sequence 354, App
94	27	52.9	344	6	US-10-878-556A-123	Sequence 123, App
95	27	52.9	351	6	US-10-467-657-8316	Sequence 8316, Ap
96	27	52.9	373	6	US-10-467-657-5582	Sequence 5582, Ap
97	27	52.9	409	6	US-10-467-657-4220	Sequence 4220, Ap
98	27	52.9	409	6	US-10-467-657-7088	Sequence 7088, Ap
99	27	52.9	418	6	US-10-793-626-1288	Sequence 1288, Ap
100	27	52.9	434	7	US-11-055-822-794	Sequence 794, App

ALIGNMENTS

RESULT 1

US-11-055-822-842

; Sequence 842, Application US/11055822

; Publication No. US20050260707A1

; GENERAL INFORMATION:

; APPLICANT: Pompejus, Markus

; APPLICANT: Kroger, Burkhard

; APPLICANT: Schroder, Hartwig

; APPLICANT: Zelder, Oskar

; APPLICANT: Haberhauer, Gregor

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING

; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

; FILE REFERENCE: BGI-121CPCN

; CURRENT APPLICATION NUMBER: US/11/055,822

; CURRENT FILING DATE: 2005-02-11

; PRIOR APPLICATION NUMBER: 09/606,740

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: 60/141,031

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; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 842
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-842

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Query Match          64.7%; Score 33; DB 7; Length 359;
Best Local Similarity 60.0%; Pred. No. 23;
Matches      6; Conservative    2; Mismatches    2; Indels      0; Gaps      0;

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Qy      1 VITTDSDGNE 10
        |  ||:||||:
Db      78 VSLTDADGND 87

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Search completed: December  8, 2005, 08:35:41
Job time : 6.90909 secs

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OM protein - protein search, using sw model

Run on: December 8, 2005, 08:15:47 ; Search time 101.364 Seconds
(without alignments)
41.221 Million cell updates/sec

Title: US-10-789-494B-1
Perfect score: 51
Sequence: 1 VITTDSDGNE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	51	100.0	10	5	US-10-789-494B-1	Sequence 1, Appli
2	51	100.0	151	5	US-10-789-494B-9	Sequence 9, Appli
3	43	84.3	317	6	US-11-097-143-30096	Sequence 30096, A
4	39	76.5	475	6	US-11-097-143-13803	Sequence 13803, A
5	39	76.5	534	4	US-10-046-232-22	Sequence 22, Appl
6	39	76.5	534	5	US-10-940-954-22	Sequence 22, Appl
7	39	76.5	559	4	US-10-046-232-20	Sequence 20, Appl
8	39	76.5	559	5	US-10-940-954-20	Sequence 20, Appl
9	39	76.5	636	4	US-10-408-765A-2973	Sequence 2973, Ap
10	38	74.5	437	4	US-10-369-493-6306	Sequence 6306, Ap
11	38	74.5	437	4	US-10-602-268-21	Sequence 21, Appl

12	38	74.5	450	4	US-10-148-884-4	Sequence 4, Appli
13	38	74.5	608	4	US-10-148-884-2	Sequence 2, Appli
14	38	74.5	953	3	US-09-884-696-3	Sequence 3, Appli
15	38	74.5	953	4	US-10-148-884-5	Sequence 5, Appli
16	37	72.5	129	3	US-09-731-660A-3	Sequence 3, Appli
17	37	72.5	508	3	US-09-731-660A-1	Sequence 1, Appli
18	37	72.5	508	3	US-09-757-415A-1	Sequence 1, Appli
19	37	72.5	508	4	US-10-146-473-67	Sequence 67, Appl
20	37	72.5	521	4	US-10-276-774-2192	Sequence 2192, Ap
21	37	72.5	862	3	US-09-738-626-3956	Sequence 3956, Ap
22	37	72.5	862	5	US-10-494-672-308	Sequence 308, App
23	37	72.5	942	4	US-10-437-963-198719	Sequence 198719,
24	37	72.5	1184	4	US-10-437-963-198716	Sequence 198716,
25	36	70.6	113	4	US-10-437-963-181695	Sequence 181695,
26	36	70.6	212	5	US-10-501-282-5738	Sequence 5738, Ap
27	36	70.6	230	3	US-09-793-708-17	Sequence 17, Appl
28	36	70.6	230	4	US-10-201-365-21	Sequence 21, Appl
29	36	70.6	230	4	US-10-160-539-17	Sequence 17, Appl
30	36	70.6	230	5	US-10-468-828-17	Sequence 17, Appl
31	36	70.6	230	5	US-10-846-335-17	Sequence 17, Appl
32	36	70.6	256	5	US-10-501-282-5740	Sequence 5740, Ap
33	36	70.6	781	4	US-10-282-122A-49736	Sequence 49736, A
34	36	70.6	924	5	US-10-450-763-58411	Sequence 58411, A
35	36	70.6	1481	4	US-10-050-763-1	Sequence 1, Appli
36	36	70.6	2402	4	US-10-661-809-20	Sequence 20, Appl
37	35	68.6	70	4	US-10-425-115-225379	Sequence 225379,
38	35	68.6	86	4	US-10-425-115-225376	Sequence 225376,
39	35	68.6	96	4	US-10-425-115-246405	Sequence 246405,
40	35	68.6	112	4	US-10-425-115-225380	Sequence 225380,
41	35	68.6	177	5	US-10-660-811A-184	Sequence 184, App
42	35	68.6	202	4	US-10-437-963-106705	Sequence 106705,
43	35	68.6	324	4	US-10-320-797-3094	Sequence 3094, Ap
44	35	68.6	364	4	US-10-282-122A-59693	Sequence 59693, A
45	35	68.6	475	4	US-10-369-493-12784	Sequence 12784, A
46	35	68.6	498	4	US-10-424-599-196154	Sequence 196154,
47	35	68.6	587	4	US-10-425-115-283525	Sequence 283525,
48	35	68.6	625	4	US-10-661-809-19	Sequence 19, Appl
49	35	68.6	772	6	US-11-097-143-31401	Sequence 31401, A
50	35	68.6	833	4	US-10-282-122A-52796	Sequence 52796, A
51	35	68.6	899	6	US-11-097-143-23256	Sequence 23256, A
52	35	68.6	899	6	US-11-097-143-23259	Sequence 23259, A
53	35	68.6	914	4	US-10-369-493-1851	Sequence 1851, Ap
54	35	68.6	1132	5	US-10-732-923-3315	Sequence 3315, Ap
55	35	68.6	1166	5	US-10-732-923-3316	Sequence 3316, Ap
56	35	68.6	1572	4	US-10-282-122A-69415	Sequence 69415, A
57	35	68.6	2468	4	US-10-246-330-4	Sequence 4, Appli
58	35	68.6	2468	4	US-10-282-122A-66335	Sequence 66335, A
59	35	68.6	4025	4	US-10-437-963-193926	Sequence 193926,
60	35	68.6	6642	4	US-10-369-493-5013	Sequence 5013, Ap
61	34	66.7	41	4	US-10-437-963-106353	Sequence 106353,
62	34	66.7	42	4	US-10-424-599-221238	Sequence 221238,
63	34	66.7	103	5	US-10-473-757-2	Sequence 2, Appli
64	34	66.7	119	4	US-10-437-963-204546	Sequence 204546,
65	34	66.7	155	4	US-10-437-963-171304	Sequence 171304,
66	34	66.7	199	4	US-10-437-963-175368	Sequence 175368,
67	34	66.7	201	4	US-10-425-114-56602	Sequence 56602, A
68	34	66.7	217	4	US-10-282-122A-72946	Sequence 72946, A

69	34	66.7	217	4	US-10-282-122A-75502	Sequence 75502, A
70	34	66.7	228	3	US-09-791-171-66	Sequence 66, Appl
71	34	66.7	228	3	US-09-804-980-66	Sequence 66, Appl
72	34	66.7	228	4	US-10-620-246-66	Sequence 66, Appl
73	34	66.7	240	4	US-10-425-115-271893	Sequence 271893,
74	34	66.7	263	6	US-11-097-143-36729	Sequence 36729, A
75	34	66.7	264	4	US-10-263-367-6	Sequence 6, Appli
76	34	66.7	352	5	US-10-994-726-78	Sequence 78, Appl
77	34	66.7	354	5	US-10-450-763-48490	Sequence 48490, A
78	34	66.7	364	5	US-10-450-763-44750	Sequence 44750, A
79	34	66.7	378	4	US-10-437-963-120806	Sequence 120806,
80	34	66.7	379	5	US-10-994-726-77	Sequence 77, Appl
81	34	66.7	403	4	US-10-282-122A-61338	Sequence 61338, A
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84	34	66.7	501	4	US-10-029-386-32319	Sequence 32319, A
85	34	66.7	570	5	US-10-732-923-8437	Sequence 8437, Ap
86	34	66.7	707	4	US-10-735-098-10	Sequence 10, Appl
87	34	66.7	813	4	US-10-369-493-17101	Sequence 17101, A
88	34	66.7	813	5	US-10-732-923-7201	Sequence 7201, Ap
89	34	66.7	953	6	US-11-097-143-18594	Sequence 18594, A
90	34	66.7	973	4	US-10-276-774-2310	Sequence 2310, Ap
91	34	66.7	1285	5	US-10-450-763-46696	Sequence 46696, A
92	34	66.7	1391	4	US-10-437-963-128235	Sequence 128235,
93	34	66.7	1632	4	US-10-282-122A-49890	Sequence 49890, A
94	34	66.7	1849	4	US-10-637-544-2	Sequence 2, Appli
95	34	66.7	1849	5	US-10-819-275-2	Sequence 2, Appli
96	34	66.7	2233	5	US-10-789-400-14	Sequence 14, Appl
97	33	64.7	59	4	US-10-425-115-219643	Sequence 219643,
98	33	64.7	66	3	US-09-867-550-728	Sequence 728, App
99	33	64.7	89	4	US-10-424-599-205325	Sequence 205325,
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ALIGNMENTS

RESULT 1

US-10-789-494B-1

; Sequence 1, Application US/10789494B

; Publication No. US20050143296A1

; GENERAL INFORMATION:

; APPLICANT: TSUBOUCHI, Kozo

; APPLICANT: YAMADA, Hiromi

; TITLE OF INVENTION: EXTRACTION AND UTILIZATION OF CELL

; TITLE OF INVENTION: GROWTH-PROMOTING PEPTIDES FROM SILK PROTEIN

; FILE REFERENCE: OPS 635

; CURRENT APPLICATION NUMBER: US/10/789,494B

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: JP 2003-55048

; PRIOR FILING DATE: 2003-02-28

; NUMBER OF SEQ ID NOS: 85

; SEQ ID NO 1

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Bombyx mori

US-10-789-494B-1

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VITDSDGNE 10
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Db 1 VITDSDGNE 10

RESULT 3

US-11-097-143-30096

; Sequence 30096, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30096
; LENGTH: 317
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-30096

Query Match 84.3%; Score 43; DB 6; Length 317;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ITDSDGNE 10
||:|||||
Db 141 ITDSDGNE 149

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Job time : 104.364 secs

OM protein - protein search, using sw model

Run on: December 8, 2005, 08:07:46 ; Search time 30 Seconds
 (without alignments)
 27.559 Million cell updates/sec

Title: US-10-789-494B-1
 Perfect score: 51
 Sequence: 1 VITDSDGNE 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

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 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	39	76.5	534	2	US-10-046-232-22	Sequence 22, Appl
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4	38	74.5	926	1	US-07-908-253-2	Sequence 2, Appli
5	38	74.5	926	1	US-08-455-970A-2	Sequence 2, Appli
6	38	74.5	926	1	US-08-387-156-6	Sequence 6, Appli
7	38	74.5	926	1	US-08-694-865-6	Sequence 6, Appli
8	38	74.5	926	1	US-08-878-748-6	Sequence 6, Appli
9	38	74.5	926	1	US-08-535-837-2	Sequence 2, Appli
10	38	74.5	926	2	US-09-124-491-6	Sequence 6, Appli
11	38	74.5	926	2	US-09-383-912-6	Sequence 6, Appli

12	38	74.5	926	2	US-08-976-566-2	Sequence 2, Appli
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16	38	74.5	943	1	US-08-455-970A-10	Sequence 10, Appl
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18	38	74.5	951	1	US-08-455-970A-14	Sequence 14, Appl
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25	38	74.5	1069	1	US-07-777-715-9	Sequence 9, Appli
26	38	74.5	1069	1	US-08-170-126-4	Sequence 4, Appli
27	38	74.5	1069	2	US-08-954-418-4	Sequence 4, Appli
28	38	74.5	1098	1	US-07-777-715-7	Sequence 7, Appli
29	38	74.5	1098	1	US-08-170-126-2	Sequence 2, Appli
30	38	74.5	1098	2	US-08-954-418-2	Sequence 2, Appli
31	37	72.5	129	2	US-08-980-523-11	Sequence 11, Appl
32	37	72.5	508	2	US-08-980-523-9	Sequence 9, Appli
33	37	72.5	729	2	US-09-543-681A-8257	Sequence 8257, Ap
34	37	72.5	856	2	US-09-605-703B-2760	Sequence 2760, Ap
35	37	72.5	3290	2	US-09-328-352-5486	Sequence 5486, Ap
36	36	70.6	230	2	US-09-320-878-17	Sequence 17, Appl
37	36	70.6	230	2	US-09-141-908-21	Sequence 21, Appl
38	36	70.6	230	2	US-09-657-440-17	Sequence 17, Appl
39	36	70.6	230	2	US-09-793-708-17	Sequence 17, Appl
40	36	70.6	1481	2	US-10-050-763-1	Sequence 1, Appli
41	35	68.6	82	2	US-09-248-796A-20781	Sequence 20781, A
42	35	68.6	161	2	US-09-538-092-756	Sequence 756, App
43	35	68.6	209	2	US-09-252-991A-26544	Sequence 26544, A
44	35	68.6	332	2	US-09-248-796A-18352	Sequence 18352, A
45	35	68.6	403	2	US-09-489-039A-11910	Sequence 11910, A
46	35	68.6	664	2	US-09-107-532A-7252	Sequence 7252, Ap
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51	34	66.7	228	2	US-09-050-739-66	Sequence 66, Appl
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53	34	66.7	339	2	US-09-543-681A-7617	Sequence 7617, Ap
54	34	66.7	352	2	US-09-830-230A-78	Sequence 78, Appl
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56	33	64.7	39	2	US-09-286-691-19	Sequence 19, Appl
57	33	64.7	39	2	US-09-687-147-19	Sequence 19, Appl
58	33	64.7	182	2	US-09-540-236-2367	Sequence 2367, Ap
59	33	64.7	213	2	US-09-902-540-14656	Sequence 14656, A
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61	33	64.7	345	2	US-09-107-532A-7021	Sequence 7021, Ap
62	33	64.7	366	2	US-10-172-527A-18	Sequence 18, Appl
63	33	64.7	377	2	US-09-248-796A-20227	Sequence 20227, A
64	33	64.7	381	2	US-10-052-092-29	Sequence 29, Appl
65	33	64.7	385	2	US-09-248-796A-21836	Sequence 21836, A
66	33	64.7	463	1	US-08-853-659A-52	Sequence 52, Appl
67	33	64.7	491	2	US-09-807-258-18	Sequence 18, Appl
68	33	64.7	644	2	US-09-710-279-1436	Sequence 1436, Ap

69	33	64.7	669	2	US-09-071-035-264	Sequence 264, App
70	33	64.7	669	2	US-10-206-576-264	Sequence 264, App
71	33	64.7	698	2	US-09-538-092-151	Sequence 151, App
72	33	64.7	716	1	US-08-372-652-4	Sequence 4, Appli
73	33	64.7	716	4	PCT-US95-16311-4	Sequence 4, Appli
74	33	64.7	849	2	US-09-949-016-9522	Sequence 9522, Ap
75	33	64.7	1638	2	US-09-071-035-258	Sequence 258, App
76	33	64.7	1638	2	US-09-071-035-262	Sequence 262, App
77	33	64.7	1638	2	US-09-071-035-266	Sequence 266, App
78	33	64.7	1638	2	US-10-206-576-258	Sequence 258, App
79	33	64.7	1638	2	US-10-206-576-262	Sequence 262, App
80	33	64.7	1638	2	US-10-206-576-266	Sequence 266, App
81	33	64.7	1747	2	US-09-134-000C-5999	Sequence 5999, Ap
82	33	64.7	2233	1	US-08-569-853-1	Sequence 1, Appli
83	33	64.7	2233	1	US-08-569-853-2	Sequence 2, Appli
84	33	64.7	2233	2	US-08-987-439-1	Sequence 1, Appli
85	33	64.7	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
86	32	62.7	136	2	US-09-270-767-32469	Sequence 32469, A
87	32	62.7	136	2	US-09-270-767-47686	Sequence 47686, A
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89	32	62.7	148	2	US-09-549-108-18	Sequence 18, Appl
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91	32	62.7	148	2	US-09-549-106-18	Sequence 18, Appl
92	32	62.7	148	2	US-09-550-394-18	Sequence 18, Appl
93	32	62.7	160	2	US-09-605-703B-1532	Sequence 1532, Ap
94	32	62.7	181	2	US-09-543-681A-4179	Sequence 4179, Ap
95	32	62.7	217	2	US-09-252-991A-31584	Sequence 31584, A
96	32	62.7	234	2	US-09-902-540-13573	Sequence 13573, A
97	32	62.7	246	2	US-09-270-767-44993	Sequence 44993, A
98	32	62.7	254	2	US-09-489-039A-10109	Sequence 10109, A
99	32	62.7	281	2	US-09-107-532A-4658	Sequence 4658, Ap
100	32	62.7	366	2	US-09-605-703B-1530	Sequence 1530, Ap

ALIGNMENTS

RESULT 1

US-10-046-232-22

; Sequence 22, Application US/10046232

; Patent No. 6861243

; GENERAL INFORMATION:

; APPLICANT: Helmut SCHWAB

; APPLICANT: Anton GLIEDER

; APPLICANT: Christoph KRATKY

; APPLICANT: Ingrid DREVENY

; APPLICANT: Peter POCHLAUER

; APPLICANT: Wolfgang SKRANC

; APPLICANT: Herbert MAYRHOFER

; APPLICANT: Irma WIRTH

; APPLICANT: Rudolf NEUHOFFER

; APPLICANT: Rodolfo BONA

; TITLE OF INVENTION: New genes containing a DNA sequence coding for a hydroxynitrile lyase,

; TITLE OF INVENTION: recombinant proteins derived therefrom and having hydroxynitrile lyase activity, and use

; TITLE OF INVENTION: thereof

; FILE REFERENCE: 2001-1882A/LC/01553
; CURRENT APPLICATION NUMBER: US/10/046,232
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: A60/2001
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: A523/2001
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Hybrid protein
PamHNL5xGOX
US-10-046-232-22

Query Match 76.5%; Score 39; DB 2; Length 534;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VITTDSDGN 9
|| |||||
Db 247 VIYTDSDGN 255

Search completed: December 8, 2005, 08:17:37
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2005, 08:03:20 ; Search time 68.6364 Seconds
(without alignments)
64.015 Million cell updates/sec

Title: US-10-789-494B-1
Perfect score: 51
Sequence: 1 VITTDSDGNE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
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4	40	78.4	101	5	ABP03713	Abp03713 Human ORF
5	39	76.5	475	4	ABB62337	Abb62337 Drosophil
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20	38	74.5	926	2	AAR14482	Aar14482	LKT352. 1
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24	38	74.5	926	2	AAW79568	Aaw79568	Leukotoxi
25	38	74.5	936	2	AAR34547	Aar34547	GnRH-leuk
26	38	74.5	943	2	AAR34546	Aar34546	Somatosta
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30	38	74.5	953	2	AAR43865	Aar43865	Leukotoxi
31	38	74.5	953	2	AAR60072	Aar60072	PtxA prot
32	38	74.5	953	4	AAE04638	Aae04638	Pasteurel
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35	38	74.5	1069	2	AAR52748	Aar52748	Bovine IF
36	38	74.5	1069	2	AAW13867	Aaw13867	Chimeric
37	38	74.5	1069	3	AAB21074	Aab21074	Bovine ga
38	38	74.5	1098	2	AAR22103	Aar22103	Bovine IL
39	38	74.5	1098	2	AAR52747	Aar52747	Bovine IL
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41	38	74.5	1098	3	AAB21073	Aab21073	Bovine IL
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44	37	72.5	508	4	AAU04693	Aau04693	Human suc
45	37	72.5	508	7	ADC35101	Adc35101	Human bre
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56	36	70.6	230	6	ABG71677	Abg71677	Partial p
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58	36	70.6	230	7	ADH53460	Adh53460	Streptomy
59	36	70.6	256	6	ADB11320	Adb11320	Alloiococ
60	36	70.6	781	6	ABU21812	Abu21812	Protein e
61	36	70.6	924	4	ABG28052	Abg28052	Novel hum
62	36	70.6	1122	2	AAR64927	Aar64927	Cytadhesi
63	36	70.6	1481	8	ADM47534	Adm47534	Thermoana
64	36	70.6	2402	8	ADO84848	Ado84848	S epiderm
65	35	68.6	161	7	ADK64272	Adk64272	Disease t

66	35	68.6	177	8	ADL81912	Adl81912	P. aerugi
67	35	68.6	209	7	ABO77798	Abo77798	Pseudomon
68	35	68.6	324	7	ADB70050	Adb70050	C. neofor
69	35	68.6	364	6	ABU31769	Abu31769	Protein e
70	35	68.6	403	7	ABO65393	Abo65393	Klebsiell
71	35	68.6	475	8	ADS23751	Ads23751	Bacterial
72	35	68.6	625	8	ADO84895	Ado84895	E faecium
73	35	68.6	625	9	ADV16668	Adv16668	E. faeciu
74	35	68.6	664	7	ADC97625	Adc97625	E. faeciu
75	35	68.6	772	4	ABB68203	Abb68203	Drosophil
76	35	68.6	833	6	ABU24872	Abu24872	Protein e
77	35	68.6	899	4	ABB65489	Abb65489	Drosophil
78	35	68.6	899	4	ABB65488	Abb65488	Drosophil
79	35	68.6	914	2	AAR77274	Aar77274	ORC1 subu
80	35	68.6	914	2	AAW22224	Aaw22224	S. cerevi
81	35	68.6	914	6	ABR53642	Abr53642	Protein s
82	35	68.6	914	7	ADK64132	Adk64132	Disease t
83	35	68.6	914	8	ADN19198	Adn19198	Bacterial
84	35	68.6	1572	6	ABU41491	Abu41491	Protein e
85	35	68.6	2468	6	ABU38411	Abu38411	Protein e
86	35	68.6	2468	6	ABP59933	Abp59933	Microbial
87	35	68.6	2736	7	ABO81481	Abo81481	Pseudomon
88	35	68.6	6642	8	ADN22360	Adn22360	Bacterial
89	34	66.7	55	3	AAB34703	Aab34703	Human sec
90	34	66.7	79	3	AAG33475	Aag33475	Arabidops
91	34	66.7	103	5	ABG72805	Abg72805	Human cyt
92	34	66.7	177	7	ADM25480	Adm25480	Hyperther
93	34	66.7	188	7	ABM89977	Abm89977	Rice abio
94	34	66.7	201	8	ADX93938	Adx93938	Plant ful
95	34	66.7	217	6	ABU47578	Abu47578	Protein e
96	34	66.7	217	6	ABU45022	Abu45022	Protein e
97	34	66.7	228	2	AAW72909	Aaw72909	Mycobacte
98	34	66.7	228	2	AAY21926	Aay21926	Amino aci
99	34	66.7	263	4	ABB69979	Abb69979	Drosophil
100	34	66.7	301	7	ABO75270	Abo75270	Pseudomon

ALIGNMENTS

RESULT 1

ADU51205

ID ADU51205 standard; peptide; 10 AA.

XX

AC ADU51205;

XX

DT 24-FEB-2005 (first entry)

XX

DE Silkworm fibroin-derived fibroblast proliferation peptide 2.

XX

KW vulnerary; cell proliferation; wound healing; cell adhesion; cosmetics;
KW cell culture; fibroin.

XX

OS Bombycoidea.

OS Synthetic.

XX

PN JP2004339189-A.

XX
 PD 02-DEC-2004.
 XX
 PF 04-DEC-2003; 2003JP-00406608.
 XX
 PR 28-FEB-2003; 2003JP-00055048.
 XX
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 PA (TSUB/) TSUBOUCHI K.
 XX
 DR WPI; 2004-827614/82.
 XX
 PT New peptide having excellent cell growth promoting activity, for use as a
 PT cell growth promoter, cell adhesion agent, wound healing-promoting agent,
 PT cosmetic and cell culture base material.
 XX
 PS Claim 2; Page; 27pp; Japanese.
 XX
 CC The invention relates to a novel peptide having excellent cell growth
 CC promoting activity. The peptide of the invention demonstrates vulnerary
 CC activity and may be utilised as a cell growth promoter, cell adhesion
 CC agent, wound healing-promoting agent or cosmetic and cell culture base
 CC material. The current sequence is that of a silkworm fibroin-derived
 CC fibroblast proliferation peptide of the invention.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VITTDSDGNE 10
 |||||
 Db 1 VITTDSDGNE 10

Search completed: December 8, 2005, 08:10:37
 Job time : 73.6364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2005, 08:04:00 ; Search time 159.273 Seconds
(without alignments)
53.156 Million cell updates/sec

Title: US-10-789-494B-5
Perfect score: 75
Sequence: 1 YGWGDGGYGSDS 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	75	100.0	421	2 Q93119_ANTPE	Q93119 antheraea p
2	75	100.0	436	2 Q967T8_ANTPE	Q967t8 antheraea p
3	75	100.0	507	2 Q8ISB3_9NEOP	Q8isb3 antheraea m
4	75	100.0	2639	2 O76786_ANTPE	O76786 antheraea p
5	75	100.0	2655	2 Q964F4_ANTYA	Q964f4 antheraea y
6	55	73.3	151	2 Q95VQ0_ANTYA	Q95vq0 antheraea y
7	53	70.7	445	2 Q4X6C2_PLACH	Q4x6c2 plasmodium
8	53	70.7	479	2 Q7RKG8_PLAYO	Q7rkg8 plasmodium
9	53	70.7	479	2 Q4Z184_PLABE	Q4z184 plasmodium
10	53	70.7	480	2 Q8IDD6_PLAF7	Q8idd6 plasmodium
11	52.5	70.0	142	2 Q97LH4_CLOAB	Q97lh4 clostridium
12	52	69.3	1410	2 Q8CMJ0_SHEON	Q8cmj0 shewanella
13	52	69.3	1422	2 Q8EFU3_SHEON	Q8efu3 shewanella
14	51	68.0	169	1 GRP10_BRANA	Q05966 brassica na
15	50	66.7	599	2 Q82M54_STRAW	Q82m54 streptomyce

16	50	66.7	602	2	O87849_STRCO	O87849 streptomyce
17	50	66.7	682	2	Q87GL4_VIBPA	Q87gl4 vibrio para
18	50	66.7	848	2	Q9RK65_STRCO	Q9rk65 streptomyce
19	50	66.7	936	2	Q4I9I0_GIBZE	Q4i9i0 gibberella
20	50	66.7	1009	2	Q6CHC1_YARLI	Q6chc1 yarrowia li
21	50	66.7	1326	2	Q4Q8G0_LEIMA	Q4q8g0 leishmania
22	48	64.0	76	2	Q6FDZ6_ACIAD	Q6fdz6 acinetobact
23	48	64.0	172	2	Q953P2_9PSIT	Q953p2 amazona och
24	48	64.0	214	1	GRP2_NICSY	P27484 nicotiana s
25	48	64.0	331	2	Q8KXI0_SHIFL	Q8kxi0 shigella fl
26	47	62.7	92	2	O24350_SILLA	O24350 silene lati
27	47	62.7	374	2	Q6LPG6_PHOPR	Q6lpg6 photobacter
28	47	62.7	443	2	Q7EZ34_ORYSA	Q7ez34 oryza sativ
29	47	62.7	527	2	Q5KFM5_CRYNE	Q5kfm5 cryptococcu
30	47	62.7	546	2	Q55QJ1_CRYNE	Q55qj1 cryptococcu
31	47	62.7	1013	2	Q97C94_THEVO	Q97c94 thermoplasm
32	47	62.7	1022	2	Q82MA7_STRAW	Q82ma7 streptomyce
33	47	62.7	1408	2	Q8E833_SHEON	Q8e833 shewanella
34	46.5	62.0	252	2	Q88DQ3_PSEPK	Q88dq3 pseudomonas
35	46	61.3	157	2	Q74XC9_YERPE	Q74xc9 yersinia pe
36	46	61.3	165	2	Q40425_NICSY	Q40425 nicotiana s
37	46	61.3	181	2	Q8D1E6_YERPE	Q8dle6 yersinia pe
38	46	61.3	192	2	Q8Z1Y5_YERPE	Q8ziy5 yersinia pe
39	46	61.3	192	2	Q66FD7_YERPS	Q66fd7 yersinia ps
40	46	61.3	287	2	Q17200_BOMMO	Q17200 bombyx mori
41	46	61.3	296	2	Q6AVS5_ORYSA	Q6avs5 oryza sativ
42	46	61.3	303	2	Q17201_BOMMO	Q17201 bombyx mori
43	46	61.3	315	2	Q8IRS1_DROME	Q8irs1 drosophila
44	46	61.3	347	2	Q9GZC7_TRYCR	Q9gzc7 trypanosoma
45	46	61.3	396	2	Q8DIF7_SYNEL	Q8dif7 synechococc
46	46	61.3	460	2	Q55MV2_CRYNE	Q55mv2 cryptococcu
47	46	61.3	460	2	Q5KB79_CRYNE	Q5kb79 cryptococcu
48	46	61.3	524	2	Q8EH30_SHEON	Q8eh30 shewanella
49	46	61.3	656	2	Q7R3F3_GIALA	Q7r3f3 giardia lam
50	46	61.3	945	2	Q8X087_NEUCR	Q8x087 neurospora
51	46	61.3	1048	2	Q9VX90_DROME	Q9vx90 drosophila
52	46	61.3	1077	2	Q8IR04_DROME	Q8ir04 drosophila
53	46	61.3	1701	2	Q7SCH8_NEUCR	Q7sch8 neurospora
54	46	61.3	1742	2	Q5AVF0_EMENI	Q5avf0 aspergillus
55	45.5	60.7	138	1	FLAV_CLOBE	P00322 clostridium
56	45.5	60.7	263	2	Q6ZL79_ORYSA	Q6zl79 oryza sativ
57	45	60.0	71	2	Q612A0_CAEBR	Q612a0 caenorhabdi
58	45	60.0	71	2	Q18838_CAEL	Q18838 caenorhabdi
59	45	60.0	185	2	Q9SIX3_ARATH	Q9six3 arabidopsis
60	45	60.0	194	2	O96853_SCHHA	O96853 schistosoma
61	45	60.0	240	2	Q4WLC1_ASPFU	Q4wlc1 aspergillus
62	45	60.0	259	2	Q7QCR4_ANOGA	Q7qcr4 anopheles g
63	45	60.0	268	2	Q51K94_MAGGR	Q51k94 magnaporthe
64	45	60.0	278	2	Q7QCR3_ANOGA	Q7qcr3 anopheles g
65	45	60.0	289	2	Q9C909_ARATH	Q9c909 arabidopsis
66	45	60.0	304	2	Q7V9Z7_PROMA	Q7v9z7 prochloroco
67	45	60.0	309	2	Q9FNR1_ARATH	Q9fnr1 arabidopsis
68	45	60.0	331	2	Q8KHE9_SHIFL	Q8khe9 shigella fl
69	45	60.0	331	2	Q8KHF0_SHIDY	Q8khf0 shigella dy
70	45	60.0	331	2	Q8KXF9_ECOLI	Q8kxf9 escherichia
71	45	60.0	331	2	Q8KXG1_ECOLI	Q8kxg1 escherichia
72	45	60.0	331	2	Q8KXG2_ECOLI	Q8kxg2 escherichia

73	45	60.0	331	2	Q8KXG3_ECOLI	Q8kxg3 escherichia
74	45	60.0	331	2	Q8KXG5_SHISO	Q8kxg5 shigella so
75	45	60.0	331	2	Q8KXG6_SHISO	Q8kxg6 shigella so
76	45	60.0	331	2	Q8KXG7_SHISO	Q8kxg7 shigella so
77	45	60.0	331	2	Q8KXG9_SHISO	Q8kxg9 shigella so
78	45	60.0	331	2	Q8KXH0_SHISO	Q8kxh0 shigella so
79	45	60.0	331	2	Q8KXH1_SHIDY	Q8kxh1 shigella dy
80	45	60.0	331	2	Q8KXH2_SHIDY	Q8kxh2 shigella dy
81	45	60.0	331	2	Q8KXH3_SHIDY	Q8kxh3 shigella dy
82	45	60.0	331	2	Q8KXH5_SHIFL	Q8kxh5 shigella fl
83	45	60.0	331	2	Q8KXH6_SHIFL	Q8kxh6 shigella fl
84	45	60.0	331	2	Q8KXH7_SHIFL	Q8kxh7 shigella fl
85	45	60.0	331	2	Q8KXH8_SHIFL	Q8kxh8 shigella fl
86	45	60.0	331	2	Q8KXH9_SHIFL	Q8kxh9 shigella fl
87	45	60.0	331	2	Q8KXI1_SHIFL	Q8kxi1 shigella fl
88	45	60.0	331	2	Q8KXI2_SHIBO	Q8kxi2 shigella bo
89	45	60.0	331	2	Q8KXI3_SHIBO	Q8kxi3 shigella bo
90	45	60.0	331	2	Q8KXI4_SHIBO	Q8kxi4 shigella bo
91	45	60.0	331	2	Q8KXI5_SHIBO	Q8kxi5 shigella bo
92	45	60.0	331	2	Q8KXI6_SHIBO	Q8kxi6 shigella bo
93	45	60.0	331	2	Q8KXI7_SHIBO	Q8kxi7 shigella bo
94	45	60.0	331	2	Q8KHF1_SHIBO	Q8khf1 shigella bo
95	45	60.0	386	2	Q7PZ31_ANOGA	Q7pz31 anopheles g
96	45	60.0	408	2	Q8TVT4_METKA	Q8tvt4 methanopyru
97	45	60.0	410	2	Q52D09_MAGGR	Q52d09 magnaporthe
98	45	60.0	422	2	Q4JIR9_9BACT	Q4jir9 uncultured
99	45	60.0	498	2	Q7VI48_HELHP	Q7vi48 helicobacte
100	45	60.0	499	2	Q8DXY8_STRA5	Q8dxy8 streptococc

ALIGNMENTS

RESULT 1

Q93119_ANTPE

ID Q93119_ANTPE PRELIMINARY; PRT; 421 AA.
AC Q93119;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Antheraea pernyi fibroin (Fragment).
OS Antheraea pernyi (Chinese oak silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Saturniidae; Saturniinae; Saturniini; Antheraea.
OX NCBI_TaxID=7119;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Posterior silk glands;
RX MEDLINE=97165499; PubMed=9013260;
RA Yukuhiro K., Kanda T., Tamura T.;
RT "Preferential codon usage and two types of repetitive motifs in the
RT fibroin gene of the Chinese oak silkworm, *Antheraea pernyi*.";
RL Insect Mol. Biol. 6:89-95(1997).
DR EMBL; D83241; BAA11860.1; -; mRNA.
DR HSSP; O87916; 1JTD.
FT NON_TER 1 1

SQ SEQUENCE 421 AA; 35800 MW; 6FBA092830262D8E CRC64;

Query Match 100.0%; Score 75; DB 2; Length 421;

Best Local Similarity 100.0%; Pred. No. 0.0061;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGWGDGGYGS DS 12

|||||||

Db 48 YGWGDGGYGS DS 59

Search completed: December 8, 2005, 08:15:39

Job time : 163.273 secs

OM protein - protein search, using sw model

Run on: December 8, 2005, 08:04:51 ; Search time 25.6364 Seconds
 (without alignments)
 45.038 Million cell updates/sec

Title: US-10-789-494B-5
 Perfect score: 75
 Sequence: 1 YGWGDGGYGS DS 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Match	Query Length			
1	75	100.0	2639	2	T31328	fibroin - Chinese
2	52.5	70.0	142	2	B96972	flavodoxin [import
3	51	68.0	169	1	S38331	glycine-rich RNA-b
4	50	66.7	602	2	T35782	probable secreted
5	48	64.0	214	1	KNNT2S	glycine-rich prote
6	46	61.3	165	2	S59529	RNA-binding glycin
7	46	61.3	165	2	S41773	glycine-rich RNA-b
8	46	61.3	192	2	AE0043	probable membrane
9	45.5	60.7	138	1	FXCLEX	flavodoxin - Clost
10	45	60.0	71	2	T15836	hypothetical prote
11	45	60.0	185	2	D84538	probable glycine-r
12	45	60.0	220	2	A44805	eggshell protein p
13	45	60.0	289	2	F96770	protein RNA-bindin

14	45	60.0	1102	2	A32247	virG protein - Shi
15	44.5	59.3	1108	2	D96798	hypothetical prote
16	44	58.7	142	2	S12311	glycine-rich RNA-b
17	44	58.7	327	2	T04919	DNA-binding protei
18	44	58.7	345	2	T07839	ananain (EC 3.4.22
19	44	58.7	407	2	F85079	probable transposo
20	44	58.7	434	2	E70768	hypothetical glyci
21	44	58.7	440	2	T50662	UVB-resistance pro
22	44	58.7	751	2	F87789	protein C34G6.2 [i
23	44	58.7	4861	2	S71752	giant protein p619
24	43.5	58.0	1028	2	A96719	hypothetical prote
25	43.5	58.0	1433	2	A46053	bullous pemphigoid
26	43	57.3	160	2	F64816	ybiA protein - Esc
27	43	57.3	447	2	T00435	probable mitochond
28	43	57.3	502	2	A70582	hypothetical prote
29	43	57.3	527	2	B70700	hypothetical prote
30	43	57.3	614	2	T10862	phaseolin G-box bi
31	43	57.3	1055	2	S53597	chlorophyll a/b-bi
32	43	57.3	4836	2	T14346	herc2 protein - mo
33	42.5	56.7	1684	2	T02367	hypothetical prote
34	42	56.0	63	2	S44634	f22b7.4 protein -
35	42	56.0	150	2	T03586	glycine-rich RNA-b
36	42	56.0	193	2	S24295	chorion protein -
37	42	56.0	211	2	S21864	probable cysteine
38	42	56.0	245	2	JQ0337	allergen Der p 1 -
39	42	56.0	257	2	C84533	hypothetical prote
40	42	56.0	285	2	T31503	hypothetical prote
41	42	56.0	313	2	S47433	cathepsin L (EC 3.
42	42	56.0	319	2	A61500	allergen Der f I p
43	42	56.0	333	2	T50630	hypothetical prote
44	42	56.0	350	2	T16385	hypothetical prote
45	42	56.0	392	2	G95258	secreted 45 kd pro
46	42	56.0	392	2	B98124	general stress pro
47	42	56.0	395	2	H84765	hypothetical prote
48	42	56.0	463	2	T46290	hypothetical prote
49	42	56.0	730	2	T43317	pgl-1 protein - Ca
50	42	56.0	771	2	T29177	hypothetical prote
51	42	56.0	968	2	E90481	alpha-mannosidase
52	42	56.0	1032	2	AI1697	alpha-mannosidase
53	42	56.0	1036	2	AG1326	alpha-mannosidase
54	42	56.0	1039	2	G83748	alpha-mannosidase
55	42	56.0	1660	2	A70869	hypothetical glyci
56	41.5	55.3	23	2	A32473	histidine-rich pro
57	41	54.7	49	2	T02026	glycine-rich prote
58	41	54.7	82	2	S19774	glycine-rich prote
59	41	54.7	139	2	S31443	glycine-rich RNA-b
60	41	54.7	144	2	S77128	hypothetical prote
61	41	54.7	145	2	T01356	glycine-rich RNA b
62	41	54.7	148	2	S41772	glycine-rich RNA-b
63	41	54.7	154	2	E84468	probable glycine-r
64	41	54.7	155	2	S20846	glycine-rich prote
65	41	54.7	157	1	S14857	glycine-rich prote
66	41	54.7	158	2	T05254	probable RNA-bindi
67	41	54.7	161	2	S71453	glycine-rich RNA-b
68	41	54.7	166	2	T10463	glycine-rich prote
69	41	54.7	167	2	S71779	glycine-rich RNA-b
70	41	54.7	168	1	S12312	glycine-rich RNA-b

71	41	54.7	169	2	T10465	glycine-rich prote
72	41	54.7	173	2	S53050	RNA binding protei
73	41	54.7	175	2	S54255	probable glycine r
74	41	54.7	179	2	T05810	hypothetical prote
75	41	54.7	203	1	JQ1061	glycine-rich prote
76	41	54.7	259	2	T15126	hypothetical prote
77	41	54.7	281	2	A65219	phnJ protein - Esc
78	41	54.7	281	2	A91264	phosphonate metabo
79	41	54.7	281	2	F86104	phosphonate metabo
80	41	54.7	288	2	AE2083	phosphonate metabo
81	41	54.7	293	2	AE0420	PhnJ protein [impo
82	41	54.7	294	2	C83224	conserved hypothet
83	41	54.7	297	2	F96023	probable C-P (carb
84	41	54.7	300	2	AD2598	conserved hypothet
85	41	54.7	300	2	E97380	phnJ protein [impo
86	41	54.7	305	2	T06413	cathepsin B-like c
87	41	54.7	307	2	A32208	synaptophysin - bo
88	41	54.7	307	2	B27287	synaptophysin - ra
89	41	54.7	312	2	AC2228	hypothetical prote
90	41	54.7	313	2	A35699	synaptophysin - hu
91	41	54.7	315	2	I50706	transcription fact
92	41	54.7	346	1	S35500	heterogeneous ribo
93	41	54.7	353	2	T06466	cathepsin B-like c
94	41	54.7	356	2	S60479	cathepsin B-like c
95	41	54.7	359	2	T02011	probable cathepsin
96	41	54.7	382	2	T27076	hypothetical prote
97	41	54.7	407	2	T21956	hypothetical prote
98	41	54.7	444	2	C90704	Rhs core protein [
99	41	54.7	444	2	G85554	Rhs core protein [
100	41	54.7	532	2	S46954	transposase - Caen

ALIGNMENTS

RESULT 1

T31328

fibroin - Chinese oak silkmoth

C;Species: *Antheraea pernyi* (Chinese oak silkmoth)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T31328

R;Sezutsu, H.; Tamura, T.; Yukuhiro, K.

submitted to the EMBL Data Library, August 1998

A;Description: Characterization of the full length fibroin gene of a wild silkworm, *Antheraea pernyi*.

A;Reference number: Z20995

A;Accession: T31328

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2639 <SEZ>

A;Cross-references: UNIPROT:O76786; UNIPARC:UPI0000078D8E; EMBL:AF083334;

NID:g3450882; PID:g3450883; PIDN:AAC32606.1

C;Genetics:

A;Introns: 14/3

Query Match 100.0%; Score 75; DB 2; Length 2639;
Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 YGWGDGGYGSDS 12
        |||||
Db      257 YGWGDGGYGSDS 268
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RESULT 2

B96972

flavodoxin [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: B96972

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B96972

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-142 <KUR>

A;Cross-references: UNIPROT:Q97LH4; UNIPARC:UPI000000C9EF3; GB:AE001437;

PIDN:AAK78565.1; PID:g15023456; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC0587

C;Superfamily: flavodoxin; flavodoxin homology

C;Keywords: flavoprotein

Query Match 70.0%; Score 52.5; DB 2; Length 142;
Best Local Similarity 45.5%; Pred. No. 1.2;
Matches 10; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

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Qy      1 YGWGDG-----GYGSD 11
        |||||           |||:|
Db      91 YGWGDGQFMRDWVERMEGYGAD 112
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Search completed: December 8, 2005, 08:16:30

Job time : 28.6364 secs

OM protein - protein search, using sw model

Run on: December 8, 2005, 08:16:37 ; Search time 7.09091 Seconds
(without alignments)
9.451 Million cell updates/sec

Title: US-10-789-494B-5
Perfect score: 75
Sequence: 1 YGWGDGGYGS DS 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	42	56.0	576	7	US-11-137-465-64	Sequence 64, Appl
2	42	56.0	579	7	US-11-045-802-32	Sequence 32, Appl
3	42	56.0	579	7	US-11-045-802-33	Sequence 33, Appl
4	42	56.0	634	7	US-11-137-465-63	Sequence 63, Appl
5	40	53.3	27	6	US-10-939-890-352	Sequence 352, App
6	40	53.3	27	6	US-10-939-890-828	Sequence 828, App
7	40	53.3	397	6	US-10-467-657-3814	Sequence 3814, Ap
8	39	52.0	123	6	US-10-467-657-8536	Sequence 8536, Ap
9	39	52.0	411	7	US-11-092-140-114	Sequence 114, App

10	39	52.0	488	7	US-11-092-140-110	Sequence 110, App
11	38.5	51.3	488	6	US-10-821-234-1000	Sequence 1000, Ap
12	38	50.7	37	7	US-11-110-424-16	Sequence 16, Appl
13	38	50.7	42	7	US-11-110-424-15	Sequence 15, Appl
14	38	50.7	2725	7	US-11-113-424-52	Sequence 52, Appl
15	37.5	50.0	390	6	US-10-821-234-1053	Sequence 1053, Ap
16	37	49.3	11	7	US-11-035-546-18	Sequence 18, Appl
17	37	49.3	229	6	US-10-689-742-38	Sequence 38, Appl
18	37	49.3	262	6	US-10-689-742-65	Sequence 65, Appl
19	37	49.3	522	7	US-11-080-991-104	Sequence 104, App
20	37	49.3	658	6	US-10-467-657-4160	Sequence 4160, Ap
21	37	49.3	660	6	US-10-878-556A-102	Sequence 102, App
22	37	49.3	674	6	US-10-821-234-965	Sequence 965, App
23	36	48.0	346	6	US-10-878-556A-58	Sequence 58, Appl
24	36	48.0	486	6	US-10-821-234-1063	Sequence 1063, Ap
25	36	48.0	544	6	US-10-821-234-889	Sequence 889, App
26	36	48.0	760	7	US-11-186-284-55	Sequence 55, Appl
27	36	48.0	2516	6	US-10-647-956A-2	Sequence 2, Appli
28	35	46.7	41	7	US-11-098-674-17	Sequence 17, Appl
29	35	46.7	120	6	US-10-821-234-1243	Sequence 1243, Ap
30	35	46.7	211	7	US-11-089-551A-19	Sequence 19, Appl
31	35	46.7	212	7	US-11-089-551A-21	Sequence 21, Appl
32	35	46.7	237	7	US-11-054-515-1906	Sequence 1906, Ap
33	35	46.7	237	7	US-11-054-515-2003	Sequence 2003, Ap
34	35	46.7	237	7	US-11-054-515-2005	Sequence 2005, Ap
35	35	46.7	237	7	US-11-054-515-2017	Sequence 2017, Ap
36	35	46.7	237	7	US-11-054-515-2019	Sequence 2019, Ap
37	35	46.7	237	7	US-11-054-515-2020	Sequence 2020, Ap
38	35	46.7	237	7	US-11-054-515-2027	Sequence 2027, Ap
39	35	46.7	237	7	US-11-054-515-2028	Sequence 2028, Ap
40	35	46.7	237	7	US-11-054-515-2040	Sequence 2040, Ap
41	35	46.7	237	7	US-11-054-515-2043	Sequence 2043, Ap
42	35	46.7	237	7	US-11-054-515-2104	Sequence 2104, Ap
43	35	46.7	237	7	US-11-054-515-2110	Sequence 2110, Ap
44	35	46.7	237	7	US-11-054-515-2111	Sequence 2111, Ap
45	35	46.7	237	7	US-11-054-515-2114	Sequence 2114, Ap
46	35	46.7	237	7	US-11-054-515-2115	Sequence 2115, Ap
47	35	46.7	237	7	US-11-054-515-2118	Sequence 2118, Ap
48	35	46.7	238	7	US-11-054-515-2053	Sequence 2053, Ap
49	35	46.7	239	7	US-11-054-515-1882	Sequence 1882, Ap
50	35	46.7	239	7	US-11-054-515-1922	Sequence 1922, Ap
51	35	46.7	241	7	US-11-054-515-1577	Sequence 1577, Ap
52	35	46.7	241	7	US-11-054-515-1887	Sequence 1887, Ap
53	35	46.7	241	7	US-11-054-515-1889	Sequence 1889, Ap
54	35	46.7	241	7	US-11-054-515-1901	Sequence 1901, Ap
55	35	46.7	241	7	US-11-054-515-1932	Sequence 1932, Ap
56	35	46.7	241	7	US-11-054-515-1948	Sequence 1948, Ap
57	35	46.7	241	7	US-11-054-515-2054	Sequence 2054, Ap
58	35	46.7	242	7	US-11-054-515-1580	Sequence 1580, Ap
59	35	46.7	242	7	US-11-054-515-1915	Sequence 1915, Ap
60	35	46.7	243	7	US-11-054-515-1883	Sequence 1883, Ap
61	35	46.7	243	7	US-11-054-515-1935	Sequence 1935, Ap
62	35	46.7	243	7	US-11-054-515-1943	Sequence 1943, Ap
63	35	46.7	243	7	US-11-054-515-1945	Sequence 1945, Ap
64	35	46.7	243	7	US-11-054-515-2063	Sequence 2063, Ap
65	35	46.7	243	7	US-11-054-515-2064	Sequence 2064, Ap
66	35	46.7	244	7	US-11-054-515-82	Sequence 82, Appl

67	35	46.7	244	7	US-11-054-515-164	Sequence 164, App
68	35	46.7	244	7	US-11-054-515-261	Sequence 261, App
69	35	46.7	244	7	US-11-054-515-280	Sequence 280, App
70	35	46.7	244	7	US-11-054-515-1881	Sequence 1881, Ap
71	35	46.7	245	7	US-11-054-515-1291	Sequence 1291, Ap
72	35	46.7	245	7	US-11-054-515-1900	Sequence 1900, Ap
73	35	46.7	245	7	US-11-054-515-1902	Sequence 1902, Ap
74	35	46.7	246	7	US-11-054-515-1920	Sequence 1920, Ap
75	35	46.7	246	7	US-11-054-515-2062	Sequence 2062, Ap
76	35	46.7	247	7	US-11-054-515-969	Sequence 969, App
77	35	46.7	247	7	US-11-054-515-1177	Sequence 1177, Ap
78	35	46.7	247	7	US-11-054-515-1923	Sequence 1923, Ap
79	35	46.7	247	7	US-11-054-515-3240	Sequence 3240, Ap
80	35	46.7	247	7	US-11-054-515-3242	Sequence 3242, Ap
81	35	46.7	248	6	US-10-512-184-32	Sequence 32, Appl
82	35	46.7	248	7	US-11-054-515-1004	Sequence 1004, Ap
83	35	46.7	248	7	US-11-054-515-1008	Sequence 1008, Ap
84	35	46.7	248	7	US-11-054-515-1104	Sequence 1104, Ap
85	35	46.7	248	7	US-11-054-515-1385	Sequence 1385, Ap
86	35	46.7	248	7	US-11-054-515-1421	Sequence 1421, Ap
87	35	46.7	248	7	US-11-054-515-1446	Sequence 1446, Ap
88	35	46.7	248	7	US-11-054-515-1700	Sequence 1700, Ap
89	35	46.7	248	7	US-11-054-515-1717	Sequence 1717, Ap
90	35	46.7	248	7	US-11-054-515-1719	Sequence 1719, Ap
91	35	46.7	248	7	US-11-054-515-1733	Sequence 1733, Ap
92	35	46.7	248	7	US-11-054-515-1737	Sequence 1737, Ap
93	35	46.7	248	7	US-11-054-515-1771	Sequence 1771, Ap
94	35	46.7	248	7	US-11-054-515-1778	Sequence 1778, Ap
95	35	46.7	248	7	US-11-054-515-1876	Sequence 1876, Ap
96	35	46.7	248	7	US-11-054-515-1879	Sequence 1879, Ap
97	35	46.7	249	7	US-11-054-515-414	Sequence 414, App
98	35	46.7	249	7	US-11-054-515-918	Sequence 918, App
99	35	46.7	249	7	US-11-054-515-919	Sequence 919, App
100	35	46.7	249	7	US-11-054-515-926	Sequence 926, App

ALIGNMENTS

RESULT 1

US-11-137-465-64

; Sequence 64, Application US/11137465
; Publication No. US20050255558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226

; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-64

Query Match 56.0%; Score 42; DB 7; Length 576;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

Qy 2 GWGDGGY----GSD 11
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Db 441 GWGDIGYSFVVGSD 454

RESULT 5

US-10-939-890-352
; Sequence 352, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03

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; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 352
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-352

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Query Match          53.3%;  Score 40;  DB 6;  Length 27;
Best Local Similarity 66.7%;  Pred. No. 2.9;
Matches      6;  Conservative    1;  Mismatches    2;  Indels      0;  Gaps      0;

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Qy      1 YGWGDGGYG 9
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Db     17 GWADGGGG 25

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RESULT 12

US-11-110-424-16

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; Sequence 16, Application US/11110424
; Publication No. US20050261479A1
; GENERAL INFORMATION:
;   APPLICANT: Hoffmann, Christian K
;   APPLICANT: Keller, Karsten
;   TITLE OF INVENTION: A Method for Purifying and Recovering Silk Proteins Using
;   TITLE OF INVENTION: Magnetic Affinity Separation
;   FILE REFERENCE: CL2418 US NA
;   CURRENT APPLICATION NUMBER: US/11/110,424
;   CURRENT FILING DATE: 2005-04-20
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: One of the repeat sequences representing spider silk
analog
;   OTHER INFORMATION: protein DP-2
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (34)..(37)
;   OTHER INFORMATION: The alanine residues at positions 34 to 37 may optionally
be
;   OTHER INFORMATION: present or absent.
US-11-110-424-16

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Query Match          50.7%;  Score 38;  DB 7;  Length 37;

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Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GWGDGGYG 9
|:| |||
Db 9 GYGPGGYG 16

Search completed: December 8, 2005, 08:35:42
Job time : 8.09091 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2005, 08:15:47 ; Search time 121.636 Seconds
(without alignments)
41.221 Million cell updates/sec

Title: US-10-789-494B-5
Perfect score: 75
Sequence: 1 YGWGDGGYGS DS 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	75	100.0	12	5	US-10-789-494B-5	Sequence 5, Appli
2	75	100.0	12	5	US-10-789-494B-62	Sequence 62, Appl
3	75	100.0	14	5	US-10-789-494B-32	Sequence 32, Appl
4	75	100.0	21	5	US-10-789-494B-30	Sequence 30, Appl
5	75	100.0	21	5	US-10-789-494B-34	Sequence 34, Appl
6	75	100.0	21	5	US-10-789-494B-37	Sequence 37, Appl
7	75	100.0	21	5	US-10-789-494B-44	Sequence 44, Appl
8	75	100.0	22	5	US-10-789-494B-36	Sequence 36, Appl
9	75	100.0	22	5	US-10-789-494B-40	Sequence 40, Appl
10	75	100.0	22	5	US-10-789-494B-42	Sequence 42, Appl
11	75	100.0	22	5	US-10-789-494B-53	Sequence 53, Appl

12	75	100.0	45	5	US-10-789-494B-25	Sequence 25, Appl
13	71	94.7	21	5	US-10-789-494B-35	Sequence 35, Appl
14	70	93.3	21	5	US-10-789-494B-45	Sequence 45, Appl
15	69	92.0	21	5	US-10-789-494B-46	Sequence 46, Appl
16	68	90.7	21	5	US-10-789-494B-39	Sequence 39, Appl
17	63.5	84.7	25	5	US-10-789-494B-48	Sequence 48, Appl
18	59	78.7	22	5	US-10-789-494B-52	Sequence 52, Appl
19	55	73.3	23	5	US-10-789-494B-28	Sequence 28, Appl
20	53	70.7	21	5	US-10-789-494B-51	Sequence 51, Appl
21	52	69.3	114	4	US-10-437-963-174027	Sequence 174027,
22	51	68.0	170	5	US-10-739-930-6860	Sequence 6860, Ap
23	50	66.7	599	4	US-10-156-761-9345	Sequence 9345, Ap
24	48	64.0	23	5	US-10-789-494B-49	Sequence 49, Appl
25	48	64.0	85	4	US-10-424-599-209214	Sequence 209214,
26	48	64.0	129	4	US-10-425-114-69985	Sequence 69985, A
27	48	64.0	163	4	US-10-767-701-45098	Sequence 45098, A
28	48	64.0	472	4	US-10-425-115-316355	Sequence 316355,
29	48	64.0	493	4	US-10-425-114-68940	Sequence 68940, A
30	48	64.0	494	4	US-10-425-114-68603	Sequence 68603, A
31	47	62.7	16	5	US-10-789-494B-41	Sequence 41, Appl
32	47	62.7	17	5	US-10-789-494B-26	Sequence 26, Appl
33	47	62.7	17	5	US-10-789-494B-64	Sequence 64, Appl
34	47	62.7	183	4	US-10-425-115-289352	Sequence 289352,
35	47	62.7	462	4	US-10-424-599-207928	Sequence 207928,
36	47	62.7	806	4	US-10-220-480-42	Sequence 42, Appl
37	47	62.7	806	4	US-10-220-481-147	Sequence 147, App
38	47	62.7	998	4	US-10-369-493-13474	Sequence 13474, A
39	47	62.7	1022	4	US-10-156-761-9292	Sequence 9292, Ap
40	46	61.3	238	5	US-10-476-264-112	Sequence 112, App
41	46	61.3	256	4	US-10-437-963-194431	Sequence 194431,
42	46	61.3	671	4	US-10-437-963-109378	Sequence 109378,
43	46	61.3	1048	6	US-11-097-143-19395	Sequence 19395, A
44	45	60.0	100	4	US-10-767-701-42596	Sequence 42596, A
45	45	60.0	133	4	US-10-424-599-281181	Sequence 281181,
46	45	60.0	168	4	US-10-425-115-264232	Sequence 264232,
47	45	60.0	1004	4	US-10-156-761-14806	Sequence 14806, A
48	44.5	59.3	157	4	US-10-424-599-158770	Sequence 158770,
49	44.5	59.3	636	4	US-10-424-599-225665	Sequence 225665,
50	44.5	59.3	1103	5	US-10-739-930-6660	Sequence 6660, Ap
51	44	58.7	91	4	US-10-424-599-162821	Sequence 162821,
52	44	58.7	120	4	US-10-425-115-268850	Sequence 268850,
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65	44	58.7	318	4	US-10-225-066A-390	Sequence 390, App
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67	44	58.7	318	4	US-10-412-699B-96	Sequence 96, Appl
68	44	58.7	318	5	US-10-495-918-130	Sequence 130, App

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88	44	58.7	776	4	US-10-424-599-180732	Sequence 180732,
89	44	58.7	1170	4	US-10-369-493-3852	Sequence 3852, Ap
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91	44	58.7	4861	3	US-09-919-497-70	Sequence 70, Appl
92	44	58.7	4861	4	US-10-097-534-26	Sequence 26, Appl
93	44	58.7	4861	4	US-10-146-473-49	Sequence 49, Appl
94	44	58.7	4861	5	US-10-287-436A-486	Sequence 486, App
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96	44	58.7	4899	6	US-11-097-143-24447	Sequence 24447, A
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ALIGNMENTS

RESULT 1

US-10-789-494B-5

; Sequence 5, Application US/10789494B

; Publication No. US20050143296A1

; GENERAL INFORMATION:

; APPLICANT: TSUBOUCHI, Kozo

; APPLICANT: YAMADA, Hiromi

; TITLE OF INVENTION: EXTRACTION AND UTILIZATION OF CELL

; TITLE OF INVENTION: GROWTH-PROMOTING PEPTIDES FROM SILK PROTEIN

; FILE REFERENCE: OPS 635

; CURRENT APPLICATION NUMBER: US/10/789,494B

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: JP 2003-55048

; PRIOR FILING DATE: 2003-02-28

; NUMBER OF SEQ ID NOS: 85

; SEQ ID NO 5

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Antheraea yamamai

US-10-789-494B-5

Query Match 100.0%; Score 75; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGWGDGGYGS DS 12
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Db 1 YGWGDGGYGS DS 12

RESULT 21

US-10-437-963-174027

; Sequence 174027, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 174027

; LENGTH: 114

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_72008C.1.pep

US-10-437-963-174027

Query Match 69.3%; Score 52; DB 4; Length 114;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGWGDGGY G 9
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Db 78 YGWGDGCGY G 86

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OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	43	57.3	135	2	US-09-270-767-32080	Sequence 32080, A
4	43	57.3	286	2	US-09-640-211A-920	Sequence 920, App
5	43	57.3	527	2	US-09-712-363-156	Sequence 156, App
6	42.5	56.7	274	2	US-09-976-594-417	Sequence 417, App
7	42.5	56.7	378	2	US-10-164-595-2	Sequence 2, Appli
8	42	56.0	24	1	US-08-482-142-25	Sequence 25, Appl
9	42	56.0	24	1	US-08-482-142-88	Sequence 88, Appl
10	42	56.0	24	1	US-08-478-572-25	Sequence 25, Appl
11	42	56.0	24	1	US-08-478-572-88	Sequence 88, Appl

12	42	56.0	24	2	US-08-484-296-25	Sequence 25, Appl
13	42	56.0	24	2	US-08-484-296-88	Sequence 88, Appl
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49	42	56.0	485	2	US-09-651-941-9	Sequence 9, Appli
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51	42	56.0	508	2	US-09-655-270A-9	Sequence 9, Appli
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53	41.5	55.3	423	2	US-09-568-102-10	Sequence 10, Appl
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57	41.5	55.3	423	2	US-09-568-472-10	Sequence 10, Appl
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63	41	54.7	290	2	US-09-489-039A-8482	Sequence 8482, Ap
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65	41	54.7	300	2	US-09-902-540-16824	Sequence 16824, A
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68	41	54.7	478	2	US-09-605-703B-2160	Sequence 2160, Ap

69	41	54.7	526	2	US-09-489-039A-10347	Sequence 10347, A
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76	40	53.3	264	2	US-09-431-887-24	Sequence 24, Appl
77	40	53.3	270	2	US-09-270-767-41818	Sequence 41818, A
78	40	53.3	341	1	US-08-538-711A-8	Sequence 8, Appli
79	40	53.3	341	2	US-08-725-027-8	Sequence 8, Appli
80	40	53.3	341	2	US-09-542-552-8	Sequence 8, Appli
81	40	53.3	353	1	US-08-538-711A-7	Sequence 7, Appli
82	40	53.3	353	2	US-08-725-027-7	Sequence 7, Appli
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92	40	53.3	1841	1	US-08-804-227C-6	Sequence 6, Appli
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96	39.5	52.7	755	2	US-09-107-433-4628	Sequence 4628, Ap
97	39.5	52.7	1088	2	US-09-130-242-2	Sequence 2, Appli
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99	39.5	52.7	1088	2	US-09-949-016-6935	Sequence 6935, Ap
100	39.5	52.7	1091	2	US-09-949-016-8595	Sequence 8595, Ap

ALIGNMENTS

RESULT 1

US-09-270-767-33522

; Sequence 33522, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 33522

; LENGTH: 158

; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*

US-09-270-767-33522

Query Match 61.3%; Score 46; DB 2; Length 158;
Best Local Similarity 70.0%; Pred. No. 31;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGWGDGGYGS 10
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Db 78 FGWGYGGYAS 87

RESULT 7

US-10-164-595-2

; Sequence 2, Application US/10164595

; Patent No. 6657054

; GENERAL INFORMATION:

; APPLICANT: OriGene Technologies, Inc

; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides

; FILE REFERENCE: 1U 103 R1

; CURRENT APPLICATION NUMBER: US/10/164,595

; CURRENT FILING DATE: 2002-06-10

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-164-595-2

Query Match 56.7%; Score 42.5; DB 2; Length 378;

Best Local Similarity 64.3%; Pred. No. 2.2e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

Qy 1 YGWGDGGY---GSD 11
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Db 260 YGGGDGGYNGFGGD 273

RESULT 8

US-08-482-142-25

; Sequence 25, Application US/08482142

; Patent No. 5820862

; GENERAL INFORMATION:

; APPLICANT: Garman, Richard

; APPLICANT: Greenstein, Julia

; APPLICANT: Kuo, Mei-chang

; APPLICANT: Rogers, Bruce

; APPLICANT: Franzen, Henry

; APPLICANT: Chen, Xian

; APPLICANT: Evans, Sean

; APPLICANT: Shaked, Ze'ev

; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS

; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)

; NUMBER OF SEQUENCES: 207

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION

; STREET: 610 LINCOLN STREET

; CITY: WALTHAM

; STATE: MA

; COUNTRY: USA

; ZIP: 02154

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,142
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-482-142-25

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Best Local Similarity 85.7%; Pred. No. 18;
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Db      16 WGDNGYG 22

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RESULT 14

PCT-US95-04481-16

; Sequence 16, Application PC/TUS9504481

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of
Dust Mit

; NUMBER OF SEQUENCES: 54

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04481

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/227,772

; FILING DATE: April 14, 1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 017.5 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04481-16

Query Match 56.0%; Score 42; DB 4; Length 24;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WGDGGYG 9
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Db 16 WGDNGYG 22

Search completed: December 8, 2005, 08:17:39
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: December 8, 2005, 08:03:20 ; Search time 82.3636 Seconds
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Title: US-10-789-494B-5
Perfect score: 75
Sequence: 1 YGWGDGGYGSDS 12

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	75	100.0	14	8	ADU51180	Adu51180 Gut silkw
4	75	100.0	21	8	ADU51182	Adu51182 Gut silkw
5	75	100.0	21	8	ADU51178	Adu51178 Gut silkw
6	75	100.0	21	8	ADU51192	Adu51192 Gut silkw
7	75	100.0	21	8	ADU51185	Adu51185 Gut silkw
8	75	100.0	22	8	ADU51201	Adu51201 Gut silkw

9	75	100.0	22	8	ADU51190	Adu51190	Gut silkw
10	75	100.0	22	8	ADU51188	Adu51188	Gut silkw
11	75	100.0	22	8	ADU51184	Adu51184	Gut silkw
12	75	100.0	45	8	ADU51173	Adu51173	Gut silkw
13	75	100.0	2655	7	ADO59401	Ado59401	Antheraea
14	71	94.7	21	8	ADU51183	Adu51183	Gut silkw
15	70	93.3	21	8	ADU51193	Adu51193	Gut silkw
16	69	92.0	21	8	ADU51194	Adu51194	Gut silkw
17	68	90.7	21	8	ADU51187	Adu51187	Gut silkw
18	63.5	84.7	25	8	ADU51196	Adu51196	Gut silkw
19	59	78.7	22	8	ADU51200	Adu51200	Gut silkw
20	55	73.3	23	8	ADU51176	Adu51176	Gut silkw
21	53	70.7	21	8	ADU51199	Adu51199	Gut silkw
22	51	68.0	170	8	ADT56783	Adt56783	Plant pol
23	49	65.3	124	5	ABB98794	Abb98794	Human cla
24	49	65.3	182	9	ADW17161	Adw17161	Eucalyptu
25	48	64.0	23	8	ADU51197	Adu51197	Gut silkw
26	48	64.0	129	8	ADY14170	Ady14170	Plant ful
27	48	64.0	214	9	ADY95170	Ady95170	Protein N
28	48	64.0	304	3	AAy81991	Aay81991	Tick alle
29	48	64.0	333	6	ABB80123	Abb80123	Blo t1. 6
30	48	64.0	346	6	ABB80124	Abb80124	Blo t1 fu
31	48	64.0	493	8	ADY13125	Ady13125	Plant ful
32	48	64.0	494	8	ADY12788	Ady12788	Plant ful
33	47	62.7	16	8	ADU51189	Adu51189	Gut silkw
34	47	62.7	17	8	ADU51174	Adu51174	Gut silkw
35	47	62.7	17	8	ADU51234	Adu51234	Gut silkw
36	47	62.7	806	4	AAE10035	Aae10035	N. mening
37	47	62.7	806	4	AAU27600	Aau27600	Neisseria
38	47	62.7	806	8	ADS00590	Ads00590	N. mening
39	47	62.7	998	8	ADS24441	Ads24441	Bacterial
40	46	61.3	67	4	AAU48381	Aau48381	Propionib
41	46	61.3	67	6	ABM44900	Abm44900	Propionib
42	46	61.3	145	4	AAU67654	Aau67654	Propionib
43	46	61.3	145	6	ABM64173	Abm64173	Propionib
44	46	61.3	146	5	ABP00239	Abp00239	Human ORF
45	46	61.3	190	4	AAU67377	Aau67377	Propionib
46	46	61.3	190	6	ABM63896	Abm63896	Propionib
47	46	61.3	1048	4	ABB64201	Abb64201	Drosophil
48	45	60.0	263	3	AAG36620	Aag36620	Arabidops
49	45	60.0	273	3	AAG36619	Aag36619	Arabidops
50	45	60.0	309	3	AAG36618	Aag36618	Arabidops
51	45	60.0	408	7	ADM26698	Adm26698	Hyperther
52	45	60.0	478	7	ADE28110	Ade28110	Human NTR
53	45	60.0	498	5	ABP27193	Abp27193	Streptoco
54	45	60.0	499	8	ADV81840	Adv81840	Streptoco
55	45	60.0	509	8	ADV88426	Adv88426	Streptoco
56	45	60.0	509	8	ADV79679	Adv79679	Streptoco
57	44.5	59.3	1103	8	ADT56583	Adt56583	Plant pol
58	44	58.7	96	3	AAG44861	Aag44861	Zea mays
59	44	58.7	141	4	ABB70805	Abb70805	Drosophil
60	44	58.7	265	3	AAG41623	Aag41623	Arabidops
61	44	58.7	302	8	ADY12065	Ady12065	Plant ful
62	44	58.7	304	3	AAG41622	Aag41622	Arabidops
63	44	58.7	306	7	ABM74277	Abm74277	DNA clone
64	44	58.7	318	4	AAE01958	Aae01958	Arabidops
65	44	58.7	318	5	AAU93117	Aau93117	Arabidops

66	44	58.7	318	6	ADA15487	Ada15487	A. thalia
67	44	58.7	318	6	ADB23126	Adb23126	Environme
68	44	58.7	318	7	ADD30358	Add30358	Plant yie
69	44	58.7	318	8	ADI43787	Adi43787	Plant tra
70	44	58.7	318	8	ADO01683	Ado01683	Thalecres
71	44	58.7	330	8	ADY04395	Ady04395	Plant ful
72	44	58.7	345	7	ABM73644	Abm73644	DNA clone
73	44	58.7	345	9	ADZ45295	Adz45295	Pineapple
74	44	58.7	349	3	AAG35161	Aag35161	Zea mays
75	44	58.7	353	3	AAG35160	Aag35160	Zea mays
76	44	58.7	354	3	AAG41621	Aag41621	Arabidops
77	44	58.7	354	3	AAG46149	Aag46149	Arabidops
78	44	58.7	354	3	AAG18708	Aag18708	Arabidops
79	44	58.7	386	7	ABM86123	Abm86123	Rice abio
80	44	58.7	397	3	AAG35159	Aag35159	Zea mays
81	44	58.7	434	9	AEB91457	Aeb91457	Microbial
82	44	58.7	436	3	AAG46148	Aag46148	Arabidops
83	44	58.7	436	3	AAG18707	Aag18707	Arabidops
84	44	58.7	440	3	AAG46147	Aag46147	Arabidops
85	44	58.7	440	3	AAG18706	Aag18706	Arabidops
86	44	58.7	459	8	ADX78457	Adx78457	Plant ful
87	44	58.7	492	8	ADY13411	Ady13411	Plant ful
88	44	58.7	530	8	ADY09863	Ady09863	Plant ful
89	44	58.7	534	8	ADT60817	Adt60817	Plant pol
90	44	58.7	634	6	ADA54695	Ada54695	Human pro
91	44	58.7	1170	8	ADN21199	Adn21199	Bacterial
92	44	58.7	4861	5	AAU84280	Aau84280	Human end
93	44	58.7	4861	6	AAE32729	Aae32729	HERC1 pro
94	44	58.7	4861	7	ADC35083	Adc35083	Human bre
95	44	58.7	4861	7	ADP65241	Adp65241	Human gua
96	44	58.7	4899	4	ABB65885	Abb65885	Drosophil
97	43.5	58.0	358	8	ADX96909	Adx96909	Plant ful
98	43.5	58.0	364	8	ADX68278	Adx68278	Plant ful
99	43.5	58.0	412	8	ADX72775	Adx72775	Plant ful
100	43	57.3	36	7	ADD26136	Add26136	Silkworm

ALIGNMENTS

RESULT 1

ADU51232

ID ADU51232 standard; peptide; 12 AA.

XX

AC ADU51232;

XX

DT 24-FEB-2005 (first entry)

XX

DE Gut silkworm fibroin peptide fragment 34.

XX

KW vulnerary; cell proliferation; wound healing; cell adhesion; cosmetics;
KW cell culture; fibroin.

XX

OS Bombycoidea.

XX

PN JP2004339189-A.

XX

PD 02-DEC-2004.
 XX
 PF 04-DEC-2003; 2003JP-00406608.
 XX
 PR 28-FEB-2003; 2003JP-00055048.
 XX
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 PA (TSUB/) TSUBOUCHI K.
 XX
 DR WPI; 2004-827614/82.
 XX
 PT New peptide having excellent cell growth promoting activity, for use as a
 PT cell growth promoter, cell adhesion agent, wound healing-promoting agent,
 PT cosmetic and cell culture base material.
 XX
 PS Example 3; Page; 27pp; Japanese.
 XX
 CC The invention relates to a novel peptide having excellent cell growth
 CC promoting activity. The peptide of the invention demonstrates vulnerary
 CC activity and may be utilised as a cell growth promoter, cell adhesion
 CC agent, wound healing-promoting agent or cosmetic and cell culture base
 CC material. The current sequence is that of a gut silkworm fibroin peptide
 CC fragment of the invention which is described as being amorphous.
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 75; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGWGDGGYGSDS 12
 |||||
 Db 1 YGWGDGGYGSDS 12

RESULT 22

ADT56783

ID ADT56783 standard; protein; 170 AA.

XX

AC ADT56783;

XX

DT 13-JAN-2005 (first entry)

XX

DE Plant polypeptide, SEQ ID 6860.

XX

KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
 KW disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX

OS Viridiplantae.

XX

PN US2004216190-A1.

XX

PD 28-OCT-2004.

XX

PF 18-DEC-2003; 2003US-00739930.

XX

PR 28-APR-2003; 2003US-00424599.

PR 28-APR-2003; 2003US-00425115.

XX

PA (KOVA/) KOVALIC D K.

XX

PI Kovalic DK;

XX

DR WPI; 2004-757369/74.

XX

PT New recombinant DNA constructs useful in the field of biochemistry and
PT genetics, and in particular for producing transgenic plants with improved
PT biological characteristics.

XX

PS Claim 2; SEQ ID NO 6860; 14pp; English.

XX

CC The invention relates a recombinant DNA construct comprising a
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region
CC functional in a plant cell operably joined to a polynucleotide encoding a
CC polypeptide associated with the property, and growing the transformed
CC plant. The property is selected from improving plant cold tolerance, for
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomannan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved nitrogen
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX

SQ Sequence 170 AA;

Query Match 68.0%; Score 51; DB 8; Length 170;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 YGWDG GGYGSDS 12
          || ||||| |
Db     154 YGGGD GGYGGGS 165
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Search completed: December 8, 2005, 08:10:41
Job time : 86.3636 secs